EXHIBIT A
PENDING CLAIMS CORRELATED
WITH CLAIM NUMBERS IN SERIAL NO. 08/872,222

Former Claim 11:
11. A phosphoinositide analogue based on di-*O*-fattyacyl (or alkyl)-*sn*-glycero-3'-phospho-*myo*-inositol or di-*O*-fattyacyl (or alkyl)-*sn*-glycero-3'-phospho-*scyllo*-inositol having at least one additional hydroxyl group derivatized as a phosphate, wherein said phosphoinositide analogue incorporates one or more of the following modifying structural features:

(a) the 2-OH is rendered non-nucleophilic by derivatization or replacement; or

(b) a reporter group or conjugand is incorporated in the fatty acyl or inositol residue;

wherein the core structure and absolute stereochemistry of the unmodified di-*O*-fattyacyl (or alkyl)-*sn*-glycero-3'-phospho-*myo*-inositol phosphate or di-*O*-fattyacyl (or alkyl)-*sn*-glycero-3'-phospho-*scyllo*-inositol phosphate is maintained in said phosphoinositide analogue.

Former Claim 12:
12. The phosphoinositide analogue of claim 11, wherein said phosphoinositide analogue is a phosphoinositide-(mono-phosphate) analogue.

Former Claim 13:
13. The phosphoinositide analogue of claim 11, wherein said phosphoinositide analogue is a phosphoinositide-(di-phosphate) analogue.

Former Claim 14:
14. The phosphoinositide analogue of claim 13, wherein said phosphoinositide analogue is a PtdIns(4,5)P_2 analogue.

Former Claim 15:
15. The phosphoinositide analogue of claim 11, wherein said phosphoinositide analogue is a phosphoinositide-(poly-phosphate) analogue.

Former Claim 16:
16. The phosphoinositide analogue of claim 11, wherein the 2-OH is rendered non-nucleophilic by derivatization or replacement.

Former Claim 17:
17. The phosphoinositide analogue of claim 16, wherein the 2-OH is rendered non-nucleophilic by derivatization.

Former Claim 18:
18. The phosphoinositide analogue of claim 17, wherein the 2-OH is rendered non-nucleophilic by derivatization to form a 2-OCOR or 2-OR phosphoinositide analogue, wherein R is alkyl, substituted alkyl or alkenyl.

Former Claim 19:
19. The phosphoinositide analogue of claim 18, wherein the 2-OH is rendered non-nucleophilic by derivatization to form 2-*O*Ac.

Former Claim 20:
20. The phosphoinositide analogue of claim 18, wherein the 2-OH is rendered non-nucleophilic by derivatization to form a 2-OCOR or 2-OR phosphoinositide analogue, wherein R is CH_3.

Former Claim 21:
21. The phosphoinositide analogue of claim 18, wherein the 2-OH is rendered non-nucleophilic by derivatization to form a 2-OCOR or 2-OR phosphoinositide analogue, wherein R is ω-amino-alkyl.

Former Claim 22:
22. The phosphoinositide analogue of claim 18, wherein the 2-OH is rendered non-nucleophilic by derivatization to form a 2-OCOR or 2-OR phosphoinositide analogue, wherein R is N-substituted-ω-amino-alkyl.

Former Claim 23:
23. The phosphoinositide analogue of claim 18, wherein the 2-OH is rendered non-nucleophilic by derivatization to form a 2-OCOR or 2-OR phosphoinositide analogue, wherein R is N,N-disubstituted-ω-amino-alkyl.

Former Claim 24:
24. The phosphoinositide analogue of claim 16, wherein the 2-OH is rendered non-nucleophilic by replacement.

Former Claim 25:
25. The phosphoinositide analogue of claim 24, wherein the 2-OH is rendered non-nucleophilic by replacement to form the 2-deoxyhalo or 2-dideoxyhalo phosphoinositide analogue.

Former Claim 26:
26. The phosphoinositide analogue of claim 25, wherein the 2-OH is rendered non-nucleophilic by replacement to form the 2-deoxyfluoro phosphoinositide analogue.

Former Claim 27:
27. The phosphoinositide analogue of claim 11, wherein a reporter group or conjugand is incorporated in the fatty acyl or inositol residue.

Former Claim 28:
28. The phosphoinositide analogue of claim 27, wherein a reporter group is incorporated.

Former Claim 29:
29. The phosphoinositide analogue of claim 28, wherein the reporter group is a photoaffinity reporter group.

Former Claim 30:
30. The phosphoinositide analogue of claim 28, wherein the reporter group is a fluorescent reporter group.

Former Claim 31:
31. The phosphoinositide analogue of claim 28, wherein the reporter group is a spin probe reporter group.

Former Claim 32:
32. The phosphoinositide analogue of claim 28, wherein the reporter group is a radioactive label reporter group.

Former Claim 33:
33. The phosphoinositide analogue of claim 28, wherein the reporter group is a stable isotope label reporter group.

Former Claim 34:
34. The phosphoinositide analogue of claim 27, wherein a conjugand is incorporated.

Former Claim 35:
35. The phosphoinositide analogue of claim 34, wherein the conjugand is alkyl-C=O, ω-NH_2-alkyl-C=O, ω-NH_2-alkyl, ω-thio-(alkyl-C=O) or ω-thio-alkyl.

Former Claim 36:
36. The phosphoinositide analogue of claim 34, wherein the conjugand is suitable for linking the phosphoinositide analogue to a polymer.

Former Claim 37:
37. The phosphoinositide analogue of claim 34, wherein the conjugand is suitable for linking the phosphoinositide analogue to a chromatographic matrix.

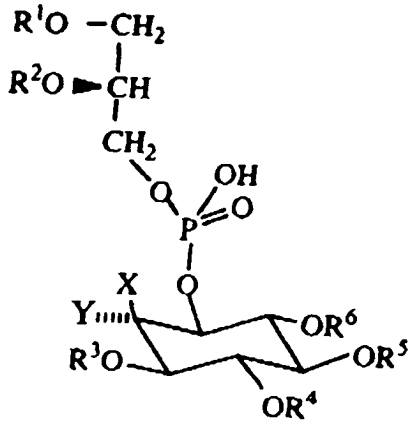
Former Claim 38:
38. The phosphoinositide analogue of claim 34, wherein the conjugand is suitable for linking the phosphoinositide analogue to a gold surface.

Former Claim 39:
39. The phosphoinositide analogue of claim 34, wherein the conjugand is suitable for linking the phosphoinositide analogue to a reporter group.

Former Claim 40:
40. The phosphoinositide analogue of claim 11, wherein one or both glycerol esters are replaced by ether bonds.

Former Claim 66:

41. A selectively *O*-protected phosphoinositide analogue obtained as a phosphodiester intermediate formed by the reaction of a selectively protected *myo*-inositol phosphate or *scyllo*-inositol phosphate and an *sn*-3-phosphatidic acid or glycero-ether analogue, wherein the said *O*-protected phosphoinositide analogue has the structure:



wherein at least one of R^3, R^4, R^5, R^6 is P(=O)(O-protecting group)$_2$,

and wherein:

(a) X = F, Cl, Br, OC(=O)R, OR, or P(=O)(O-protecting group)$_2$, and Y = H; or
X = Y = H; or

(b) X = H, and Y = F, Cl, Br, OC(=O)R, OR, or P(=O)(O-protecting group)$_2$; or

(c) X = Y = F or (=O);
where R = alkyl, especially methyl or ethyl, alkenyl, alkynyl, ω-aminoalkyl, N-substituted-ω-aminoalkyl or N,N-disubstituted-ω-aminoalkyl;

and wherein

(d) R^1 = RC(=O) or R, R^2 = R'C(=O) or R'
where R, R' = alkyl or alkenyl;

and wherein:

(e) R^3 = H, or P(=O)(O-protecting group)$_2$,

(f) R^4 = H, or P(=O)(O-protecting group)$_2$,

(g) R^5 = H, or P(=O)(O-protecting group)$_2$,

(h) R^6 = H, P(=O)(O-protecting group)$_2$, ω-aminoalkyl, ω-aminoalkenyl, ω-sulfhydrylalkyl, ω-carboxyalkyl, ω-(4-azidosalicylamido)-alkyl, alkyl-aminofluorophor, alkyl-amidofluorophor, or alkyl-fluorophor.

Former Claim 70:

42. The phosphoinositide analogue of claim 11, wherein:

(a) the 2-OH is rendered non-nucleophilic by derivatization or replacement; and

(b) a reporter group or conjugand is incorporated in the fatty acyl or inositol residue;

wherein the core structure and absolute stereochemistry of the unmodified di-*O*-fattyacyl (or alkyl)-*sn*-glycero-3'-phospho-*myo*-inositol phosphate or di-*O*-fattyacyl (or alkyl)-*sn*-glycero-3'-phospho-*scyllo*-inositol phosphate is maintained in said phosphoinositide analogue.

Former Claim 79:

43. A phosphoinositide analogue based on di-*O*-fattyacyl (or alkyl)-*sn*-glycero-3'-phospho-*myo*-inositol or di-*O*-fattyacyl (or alkyl)-*sn*-glycero-3'-phospho-*scyllo*-inositol having at least one additional hydroxyl group derivatized as a phosphate, wherein the 2-OH is rendered non-nucleophilic by derivatization or replacement and wherein the core structure and absolute stereochemistry of the unmodified di-*O*-fattyacyl (or alkyl)-*sn*-glycero-3'-phospho-*myo*-inositol phosphate or di-*O*-fattyacyl (or alkyl)-*sn*-glycero-3'-phospho-*scyllo*-inositol phosphate is maintained in said phosphoinositide analogue.

Former Claim 84:

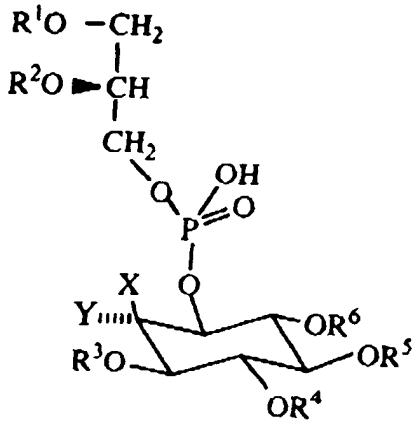
44. The phosphoinositide analogue of claim 11, wherein said phosphoinositide analogue is based on di-*O*-fattyacyl (or alkyl)-*sn*-glycero-3'-phospho-*myo*-inositol phosphate.

Former Claim 85:

45. The phosphoinositide analogue of claim 11, wherein said phosphoinositide analogue is based on di-*O*-fattyacyl (or alkyl)-*sn*-glycero-3'-phospho-*scyllo*-inositol phosphate.

Former Claim 86, Amended as shown:

46. A selectively *O*-protected phosphoinositide analogue obtained as a phosphodiester intermediate formed by the reaction of a selectively protected *myo*-inositol phosphate or *scyllo*-inositol phosphate and an *sn*-3-phosphatidic acid or glycero ether analogue, wherein the said *O*-protected phosphoinositide analogue has the structure:



wherein at least one of R^3, R^4, R^5, R^6 is P(=O)(O-protecting group)$_2$,

and wherein

(a) X = OH, and Y = H; or X = H, and Y = OH;

and wherein

(b) R^1 = RC(=O) or R, R^2 = R'C(=O) or R'
where R = alkyl, alkenyl, alkynyl, R' = ω-aminoalkyl, ω-(substitutedamino)-alkyl, ω-aminoalkenyl, ω-sulfhydrylalkyl, ω-carboxyalkyl, ω-(4-azidosalicylamido)-alkyl, ω-(substitutedamido)-alkyl, alkyl-aminofluorophor, alkyl-amidofluorophor, alkyl-fluorophor, hydroxylalkyl, or ketoalkyl; or where R'= alkyl, alkenyl, alkynyl, R = ω-aminoalkyl, ω-(substitutedamino)-alkyl, ω-aminoalkenyl, ω-sulfhydrylalkyl, ω-carboxyalkyl, ω-(4-azidosalicylamido)-alkyl, ω-(substitutedamido)-alkyl, alkyl-aminofluorophor, alkyl-amidofluorophor, alkyl-fluorophor, hydroxylalkyl, or ketoalkyl; or where R = R', except when R = R' = alkyl;

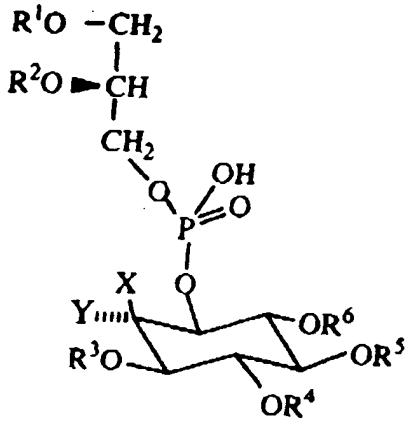
and wherein

(c) R^3 = H, or P(=O)(O-protecting group)$_2$,
(d) R^4 = H, or P(=O)(O-protecting group)$_2$,
(e) R^5 = H, or P(=O)(O-protecting group)$_2$,

(f) R^6 = H, P(=O)(O-protecting group)$_2$, , ω-aminoalkyl, ω-aminoalkenyl, ω-sulfhydrylalkyl, ω-carboxyalkyl, ω-(4-azidosalicylamido)-alkyl, alkyl-aminofluorophor, alkyl-amidofluorophor, or alkyl-fluorophor.

Former Claim 87:

47. A selectively *O*-protected phosphoinositide analogue obtained as a phosphodiester intermediate formed by the reaction of a selectively protected *myo*-inositol phosphate or *scyllo*-inositol phosphate and an *sn*-3-phosphatidic acid or glycero ether analogue, wherein the said *O*-protected phosphoinositide analogue has the structure:



wherein at least one of R^3, R^4, R^5, R^6 is P(=O)(O-protecting group)$_2$,

and wherein

(a) X = F, Cl, Br, OC(=O)R, OR, or P(=O)(O-protecting group)$_2$, and Y = H; or X = Y = H; or

(b) X = H, and Y = F, Cl, Br, OC(=O)R, OR, or P(=O)(O-protecting group)$_2$, or

(c) X = Y = F or (=O);

where R = alkyl, especially methyl or ethyl, alkenyl, alkynyl, ω-aminoalkyl, N-substituted-ω-aminoalkyl or N,N-disubstituted-ω-aminoalkyl;

and wherein

(d) R^1 = RC(=O) or R, R^2 = R'C(=O) or R'

where R = alkyl, alkenyl, alkynyl, R' = ω-aminoalkyl, ω-(substitutedamino)-alkyl, ω-aminoalkenyl, ω-sulfhydrylalkyl, ω-carboxyalkyl, ω-(4-azidosalicylamido)-alkyl, ω-(substitutedamido)-alkyl, alkyl-aminofluorophor, alkyl-amidofluorophor, alkyl-fluorophor, hydroxylalkyl, or ketoalkyl; or where R' = alkyl, alkenyl, alkynyl, R = ω-aminoalkyl, ω-(substitutedamino)-alkyl, ω-aminoalkenyl,

ω-sulfhydrylalkyl, ω-carboxyalkyl, ω-(4-azidosalicylamido)-alkyl, ω-(substitutedamido)-alkyl, alkyl-aminofluorophor, alkyl-amidofluorophor, alkyl-fluorophor, hydroxylalkyl, or ketoalkyl; or where R = R';

and wherein

(e) R^3 = H, or P(=O)(O-protecting group)$_2$,

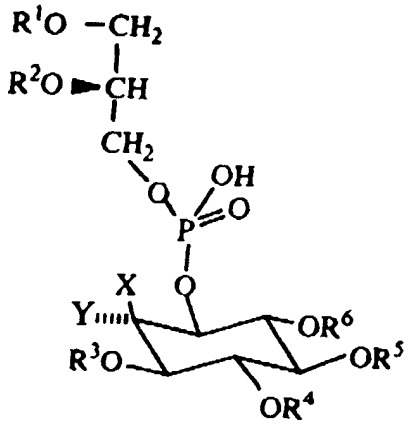
(f) R^4 = H, or P(=O)(O-protecting group)$_2$,

(g) R^5 = H, or P(=O)(O-protecting group)$_2$,

(h) R^6 = H, P(=O)(O-protecting group)$_2$, ω-aminoalkyl, ω-aminoalkenyl, ω-sulfhydrylalkyl, ω-carboxyalkyl, ω-(4-azidosalicylamido)-alkyl, alkyl-aminofluorophor, alkyl-amidofluorophor, or alkyl-fluorophor.

Former Claim 88:

48. A phosphoinositide analogue based on phosphatidylinositolphosphate, wherein the 2-OH is rendered non-nucleophilic by derivatization or replacement or wherein a reporter group or conjugand is incorporated in the fatty acyl or inositol residue; wherein the core structure and absolute stereochemistry of the unmodified phosphatidylinositolphosphate is maintained in said phosphoinositide analogue; and wherein said phosphoinositide analogue has the structure:



wherein at least one of R^3, R^4, R^5, R^6 is P(=O)(OH)$_2$,

and wherein

(a) X = F, Cl, Br, OC(=O)R, OR, or OP(=O)(OH)$_2$, and Y = H; or
X = Y = H; or

(b) X = H, and Y = F, Cl, Br, OC(=O)R, OR, or OP(=O)(OH)$_2$; or

(c) X = Y = F or (=O);
where R = alkyl, especially methyl or ethyl, alkenyl, alkynyl, ω-aminoalkyl, N-substituted-ω-aminoalkyl or N,N-disubstituted-ω-aminoalkyl;

and wherein

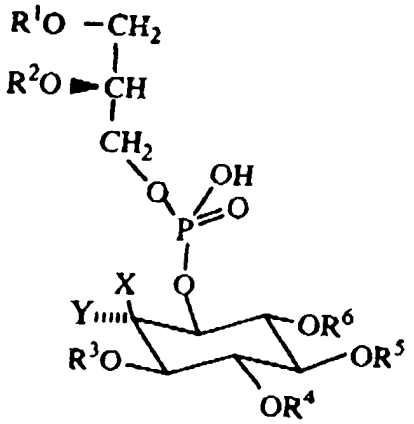
(d) R^1 = RC(=O) or R, R^2 = R'C(=O) or R'
where R, R' = alkyl or alkenyl;

and wherein

(e) R^3 = H, or $P(=O)(OH)_2$
(f) R^4 = H, or $P(=O)(OH)_2$
(g) R^5 = H, or $P(=O)(OH)_2$
(h) R^6 = H, $P(=O)(OH)_2$, ω-aminoalkyl, ω-aminoalkenyl, ω-sulfhydrylalkyl, ω-carboxyalkyl, ω-(4-azidosalicylamido)-alkyl, alkyl-aminofluorophor, alkyl-amidofluorophor, or alkyl-fluorophor.

Former Claim 89, Amended as shown:

49. A phosphoinositide analogue based on phosphatidylinositolphosphate, wherein the 2-OH is rendered non-nucleophilic by derivatization or replacement or wherein a reporter group or conjugand is incorporated in the fatty acyl or inositol residue; wherein the core structure and absolute stereochemistry of the unmodified phosphatidylinositolphosphate is maintained in said phosphoinositide analogue; and wherein said phosphoinositide analogue has the structure:



wherein at least one of R^3, R^4, R^5, R^6 is $P(=O)(OH)_2$,

and wherein

(a) X = OH, and Y = H; or X = H, and Y = OH;

and wherein

(b) R^1 = RC(=O) or R, R^2 = R'C(=O) or R'
where R = alkyl, alkenyl, alkynyl, R' = ω-aminoalkyl, ω-(substitutedamino)-alkyl, ω-aminoalkenyl, ω-sulfhydrylalkyl, ω-carboxyalkyl, ω-(4-azidosalicylamido)-alkyl, ω-(substitutedamido)-alkyl, alkyl-aminofluorophor, alkyl-amidofluorophor, alkyl-fluorophor, hydroxylalkyl, or ketoalkyl; or where R' = alkyl, alkenyl,

alkynyl, R = ω-aminoalkyl, ω-(substitutedamino)-alkyl, ω-aminoalkenyl, ω-sulfhydrylalkyl, ω-carboxyalkyl, ω-(4-azidosalicylamido)-alkyl, ω-(substitutedamido)-alkyl, alkyl-aminofluorophor, alkyl-amidofluorophor, alkyl-fluorophor, hydroxylalkyl, or ketoalkyl; or where R = R', except when R = R' = alkyl;

and wherein

(c) R^3 = H, or $P(=O)(OH)_2$

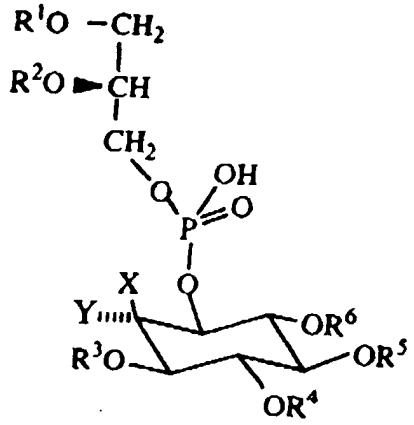
(d) R^4 = H, or $P(=O)(OH)_2$

(e) R^5 = H, or $P(=O)(OH)_2$

(f) R^6 = H, $P(=O)(OH)_2$, ω-aminoalkyl, ω-aminoalkenyl, ω-sulfhydrylalkyl, ω-carboxyalkyl, ω-(4-azidosalicylamido)-alkyl, alkyl-aminofluorophor, alkyl-amidofluorophor, or alkyl-fluorophor.

Former Claim 90:

50. A phosphoinositide analogue based on phosphatidylinositolphosphate, wherein the 2-OH is rendered non-nucleophilic by derivatization or replacement and a reporter group or conjugand is incorporated in the fatty acyl or inositol residue; wherein the core structure and absolute stereochemistry of the unmodified phosphatidylinositolphosphate is maintained in said phosphoinositide analogue; and wherein said phosphoinositide analogue has the structure:



wherein at least one of R^3, R^4, R^5, R^6 is $P(=O)(OH)_2$,

and wherein

(a) X = F, Cl, Br, OC(=O)R, OR, or $OP(=O)(OH)_2$, and Y = H; or
X = Y = H; or

(b) X = H, and Y = F, Cl, Br, OC(=O)R, OR, or $OP(=O)(OH)_2$; or

(c) X = Y = F or (=O);
where R = alkyl, especially methyl or ethyl, alkenyl, alkynyl, ω-aminoalkyl, N-substituted-ω-aminoalkyl or N,N-disubstituted-ω-aminoalkyl;

and wherein

(d) R^1 = RC(=O) or R, R^2 = R'C(=O) or R'
where R = alkyl, alkenyl, alkynyl, R' = ω-aminoalkyl, ω-(substitutedamino)-alkyl, ω-aminoalkenyl, ω-sulfhydrylalkyl, ω-carboxyalkyl, ω-(4-azidosalicylamido)-alkyl, ω-(substitutedamido)-alkyl, alkyl-aminofluorophor, alkyl-amidofluorophor, alkyl-fluorophor, hydroxylalkyl, or ketoalkyl; or where R' = alkyl, alkenyl, alkynyl, R = ω-aminoalkyl, ω-(substitutedamino)-alkyl, ω-aminoalkenyl, ω-sulfhydrylalkyl, ω-carboxyalkyl, ω-(4-azidosalicylamido)-alkyl, ω-(substitutedamido)-alkyl, alkyl-aminofluorophor, alkyl-amidofluorophor, alkyl-fluorophor, hydroxylalkyl, or ketoalkyl; or where R = R';

and wherein

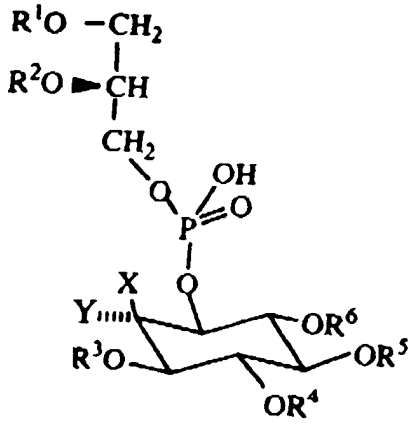
(e) R^3 = H, or $P(=O)(OH)_2$
(f) R^4 = H, or $P(=O)(OH)_2$
(g) R^5 = H, or $P(=O)(OH)_2$
(h) R^6 = H, $P(=O)(OH)_2$, ω-aminoalkyl, ω-aminoalkenyl, ω-sulfhydrylalkyl, ω-carboxyalkyl, ω-(4-azidosalicylamido)-alkyl, alkyl-aminofluorophor, alkyl-amidofluorophor, or alkyl-fluorophor.

Former Claim 91, Amended as shown:

51. Matched pairs of the 2-modified phosphatidylinositol-phosphates of claim 48 and the corresponding phosphatidylinositol-phosphate structure lacking the 2-modification, wherein X=OH and Y=H, or X=H and Y=OH.

New Claim, based upon former Claim 81, Amended:

52. The phosphoinositide analogue of claim 11, wherein said phosphoinositide analogue has the structure:



wherein at least one of R^3, R^4, R^5, R^6 is $P(=O)(OH)_2$,

and wherein

(a) X = OH, and Y = H; or X = H, and Y = OH

and wherein

(b) R^1 = RC(=O) or R, R^2 = R'C(=O) or R'
where R = alkyl, alkenyl, alkynyl, R' = ω-aminoalkyl, ω-(substitutedamino)-alkyl, ω-aminoalkenyl, ω-sulfhydrylalkyl, ω-carboxyalkyl, ω-(4-azidosalicylamido)-alkyl, ω-(substitutedamido)-alkyl, alkyl-aminofluorophor, alkyl-amidofluorophor, [alkyl-fluorophor], hydroxylalkyl, or ketoalkyl; or where R' = alkyl, alkenyl, alkynyl, R = ω-aminoalkyl, ω-(substitutedamino)-alkyl, ω-aminoalkenyl, ω-sulfhydrylalkyl, ω-carboxyalkyl, ω-(4-azidosalicylamido)-alkyl, ω-(substitutedamido)-alkyl, alkyl-aminofluorophor, alkyl-amidofluorophor, hydroxylalkyl, or ketoalkyl;

and wherein

(c) R^3 = H, or $P(=O)(OH)_2$

(d) R^4 = H, or $P(=O)(OH)_2$

(e) R^5 = H, or $P(=O)(OH)_2$

(f) R^6 = H, $P(=O)(OH)_2$, ω-aminoalkyl, ω-aminoalkenyl, ω-sulfhydrylalkyl, ω-carboxyalkyl, ω-(4-azidosalicylamido)-alkyl, alkyl-aminofluorophor, alkyl-amidofluorophor, or alkyl-fluorophor.

New Claim, supported by claim 11:

53. A phosphoinositide analogue based on di-*O*-fattyacyl (or alkyl)-*sn*-glycero-3'-phospho-*myo*-inositol or di-*O*-fattyacyl (or alkyl)-*sn*-glycero-3'-phospho-*scyllo*-inositol having at least one additional hydroxyl group derivatized as a phosphate, wherein said phosphoinositide analogue incorporates one or more of the following modifying structural features:

(a) the 2-OH is rendered non-nucleophilic by derivatization or replacement; or

(b) a conjugand suitable for linking to a reporter group, polymer, chromatographic matrix, or gold surface is incorporated in the fattyacyl or inositol residue; wherein said conjugand is selected from the group consisting of ω-aminoalkyl, ω-(substitutedamino)-alkyl, ω-aminoalkenyl, ω-sulfhydrylalkyl, ω-carboxyalkyl, hydroxylalkyl and ketoalkyl, and wherein the amino, substitutedamino, sulfhydryl, carboxyl, hydroxyl and keto functions are free and unsubstituted, or are covalently linked to a reporter group;

wherein the core structure and absolute stereochemistry of the unmodified di-*O*-fattyacyl (or alkyl)-*sn*-glycero-3'-phospho-*myo*-inositol phosphate or di-*O*-fattyacyl (or alkyl)-*sn*-glycero-3'-phospho-*scyllo*-inositol phosphate is maintained in said phosphoinositide analogue.

EXHIBIT B
PENDING CLAIMS
CONTINUATION OF SERIAL NO.08/872,222 (NUBI:004--1)

11. A phosphoinositide analogue based on di-*O*-fattyacyl (or alkyl)-*sn*-glycero-3'-phospho-*myo*-inositol or di-*O*-fattyacyl (or alkyl)-*sn*-glycero-3'-phospho-*scyllo*-inositol having at least one additional hydroxyl group derivatized as a phosphate, wherein said phosphoinositide analogue incorporates one or more of the following modifying structural features:

(a) the 2-OH is rendered non-nucleophilic by derivatization or replacement; or

(b) a reporter group or conjugand is incorporated in the fatty acyl or inositol residue;

wherein the core structure and absolute stereochemistry of the unmodified di-*O*-fattyacyl (or alkyl)-*sn*-glycero-3'-phospho-*myo*-inositol phosphate or di-*O*-fattyacyl (or alkyl)-*sn*-glycero-3'-phospho-*scyllo*-inositol phosphate is maintained in said phosphoinositide analogue.

12. The phosphoinositide analogue of claim 11, wherein said phosphoinositide analogue is a phosphoinositide-(mono-phosphate) analogue.

13. The phosphoinositide analogue of claim 11, wherein said phosphoinositide analogue is a phosphoinositide-(di-phosphate) analogue.

14. The phosphoinositide analogue of claim 13, wherein said phosphoinositide analogue is a PtdIns(4,5)P_2 analogue.

15. The phosphoinositide analogue of claim 11, wherein said phosphoinositide analogue is a phosphoinositide-(poly-phosphate) analogue.

16. The phosphoinositide analogue of claim 11, wherein the 2-OH is rendered non-nucleophilic by derivatization or replacement.

17. The phosphoinositide analogue of claim 16, wherein the 2-OH is rendered non-nucleophilic by derivatization.

18. The phosphoinositide analogue of claim 17, wherein the 2-OH is rendered non-nucleophilic by derivatization to form a 2-OCOR or 2-OR phosphoinositide analogue, wherein R is alkyl, substituted alkyl or alkenyl.

19. The phosphoinositide analogue of claim 18, wherein the 2-OH is rendered non-nucleophilic by derivatization to form 2-*O*Ac.

20. The phosphoinositide analogue of claim 18, wherein the 2-OH is rendered non-nucleophilic by derivatization to form a 2-OCOR or 2-OR phosphoinositide analogue, wherein R is CH_3.

21. The phosphoinositide analogue of claim 18, wherein the 2-OH is rendered non-nucleophilic by derivatization to form a 2-OCOR or 2-OR phosphoinositide analogue, wherein R is ω-amino-alkyl.

22. The phosphoinositide analogue of claim 18, wherein the 2-OH is rendered non-nucleophilic by derivatization to form a 2-OCOR or 2-OR phosphoinositide analogue, wherein R is N-substituted-ω-amino-alkyl.

23. The phosphoinositide analogue of claim 18, wherein the 2-OH is rendered non-nucleophilic by derivatization to form a 2-OCOR or 2-OR phosphoinositide analogue, wherein R is N,N-disubstituted-ω-amino-alkyl.

24. The phosphoinositide analogue of claim 16, wherein the 2-OH is rendered non-nucleophilic by replacement.

25. The phosphoinositide analogue of claim 24, wherein the 2-OH is rendered non-nucleophilic by replacement to form the 2-deoxyhalo or 2-dideoxyhalo phosphoinositide analogue.

26. The phosphoinositide analogue of claim 25, wherein the 2-OH is rendered non-nucleophilic by replacement to form the 2-deoxyfluoro phosphoinositide analogue.

27. The phosphoinositide analogue of claim 11, wherein a reporter group or conjugand is incorporated in the fatty acyl or inositol residue.

28. The phosphoinositide analogue of claim 27, wherein a reporter group is incorporated.

29. The phosphoinositide analogue of claim 28, wherein the reporter group is a photoaffinity reporter group.

30. The phosphoinositide analogue of claim 28, wherein the reporter group is a fluorescent reporter group.

31. The phosphoinositide analogue of claim 28, wherein the reporter group is a spin probe reporter group.

32. The phosphoinositide analogue of claim 28, wherein the reporter group is a radioactive label reporter group.

33. The phosphoinositide analogue of claim 28, wherein the reporter group is a stable isotope label reporter group.

34. The phosphoinositide analogue of claim 27, wherein a conjugand is incorporated.

35. The phosphoinositide analogue of claim 34, wherein the conjugand is alkyl-C=O, ω-NH_2-alkyl-C=O, ω-NH_2-alkyl, ω-thio-(alkyl-C=O) or ω-thio-alkyl.

36. The phosphoinositide analogue of claim 34, wherein the conjugand is suitable for linking the phosphoinositide analogue to a polymer.

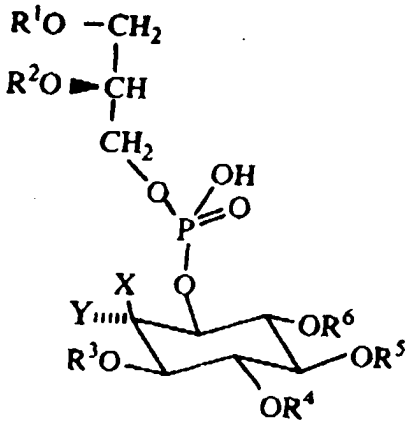
37. The phosphoinositide analogue of claim 34, wherein the conjugand is suitable for linking the phosphoinositide analogue to a chromatographic matrix.

38. The phosphoinositide analogue of claim 34, wherein the conjugand is suitable for linking the phosphoinositide analogue to a gold surface.

39. The phosphoinositide analogue of claim 34, wherein the conjugand is suitable for linking the phosphoinositide analogue to a reporter group.

40. The phosphoinositide analogue of claim 11, wherein one or both glycerol esters are replaced by ether bonds.

41. A selectively *O*-protected phosphoinositide analogue obtained as a phosphodiester intermediate formed by the reaction of a selectively protected *myo*-inositol phosphate or *scyllo*-inositol phosphate and an *sn*-3-phosphatidic acid or glycero-ether analogue, wherein the said *O*-protected phosphoinositide analogue has the structure:



wherein at least one of R^3, R^4, R^5, R^6 is P(=O)(O-protecting group)$_2$,

and wherein:

(a) X = F, Cl, Br, OC(=O)R, OR, or P(=O)(O-protecting group)$_2$, and Y = H; or
X = Y = H; or
(b) X = H, and Y = F, Cl, Br, OC(=O)R, OR, or P(=O)(O-protecting group)$_2$; or
(c) X = Y = F or (=O);
where R = alkyl, especially methyl or ethyl, alkenyl, alkynyl, ω-aminoalkyl, N-substituted-ω-aminoalkyl or N,N-disubstituted-ω-aminoalkyl;

and wherein

(d) R^1 = RC(=O) or R, R^2 = R'C(=O) or R'
where R, R' = alkyl or alkenyl;

and wherein:

(e) R^3 = H, or P(=O)(O-protecting group)$_2$,
(f) R^4 = H, or P(=O)(O-protecting group)$_2$,
(g) R^5 = H, or P(=O)(O-protecting group)$_2$,

(h) R^6 = H, P(=O)(O-protecting group)$_2$, ω-aminoalkyl, ω-aminoalkenyl, ω-sulfhydrylalkyl, ω-carboxyalkyl, ω-(4-azidosalicylamido)-alkyl, alkyl-aminofluorophor, alkyl-amidofluorophor, or alkyl-fluorophor.

42. The phosphoinositide analogue of claim 11, wherein:

(a) the 2-OH is rendered non-nucleophilic by derivatization or replacement; and

(b) a reporter group or conjugand is incorporated in the fatty acyl or inositol residue;

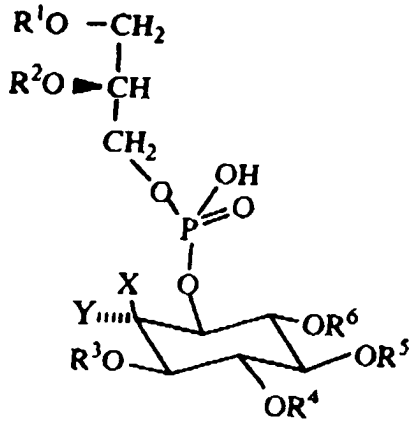
wherein the core structure and absolute stereochemistry of the unmodified di-*O*-fattyacyl (or alkyl)-*sn*-glycero-3'-phospho-*myo*-inositol phosphate or di-*O*-fattyacyl (or alkyl)-*sn*-glycero-3'-phospho-*scyllo*-inositol phosphate is maintained in said phosphoinositide analogue.

43. A phosphoinositide analogue based on di-*O*-fattyacyl (or alkyl)-*sn*-glycero-3'-phospho-*myo*-inositol or di-*O*-fattyacyl (or alkyl)-*sn*-glycero-3'-phospho-*scyllo*-inositol having at least one additional hydroxyl group derivatized as a phosphate, wherein the 2-OH is rendered non-nucleophilic by derivatization or replacement and wherein the core structure and absolute stereochemistry of the unmodified di-*O*-fattyacyl (or alkyl)-*sn*-glycero-3'-phospho-*myo*-inositol phosphate or di-*O*-fattyacyl (or alkyl)-*sn*-glycero-3'-phospho-*scyllo*-inositol phosphate is maintained in said phosphoinositide analogue.

44. The phosphoinositide analogue of claim 11, wherein said phosphoinositide analogue is based on di-*O*-fattyacyl (or alkyl)-*sn*-glycero-3'-phospho-*myo*-inositol phosphate.

45. The phosphoinositide analogue of claim 11, wherein said phosphoinositide analogue is based on di-*O*-fattyacyl (or alkyl)-*sn*-glycero-3'-phospho-*scyllo*-inositol phosphate.

46. A selectively *O*-protected phosphoinositide analogue obtained as a phosphodiester intermediate formed by the reaction of a selectively protected *myo*-inositol phosphate or *scyllo*-inositol phosphate and an *sn*-3-phosphatidic acid or glycero ether analogue, wherein the said *O*-protected phosphoinositide analogue has the structure:



wherein at least one of R^3, R^4, R^5, R^6 is P(=O)(O-protecting group)$_2$,

and wherein

(a) X = OH, and Y = H; or X = H, and Y = OH;

and wherein

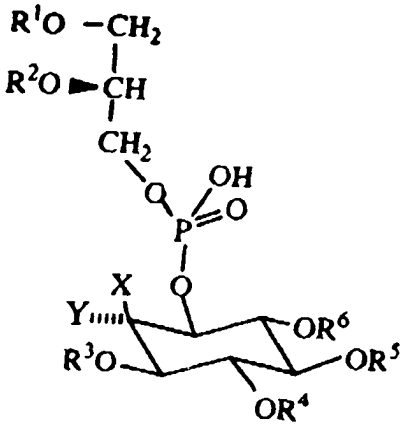
(b) R^1 = RC(=O) or R, R^2 = R'C(=O) or R'
where R = alkyl, alkenyl, alkynyl, R' = ω-aminoalkyl, ω-(substitutedamino)-alkyl, ω-aminoalkenyl, ω-sulfhydrylalkyl, ω-carboxyalkyl, ω-(4-azidosalicylamido)-alkyl, ω-(substitutedamido)-alkyl, alkyl-aminofluorophor, alkyl-amidofluorophor, alkyl-fluorophor, hydroxylalkyl, or ketoalkyl; or where R'= alkyl, alkenyl, alkynyl, R = ω-aminoalkyl, ω-(substitutedamino)-alkyl, ω-aminoalkenyl, ω-sulfhydrylalkyl, ω-carboxyalkyl, ω-(4-azidosalicylamido)-alkyl, ω-(substitutedamido)-alkyl, alkyl-aminofluorophor, alkyl-amidofluorophor, alkyl-fluorophor, hydroxylalkyl, or ketoalkyl; or where R = R', except when R = R' = alkyl;

and wherein

(c) R^3 = H, or P(=O)(O-protecting group)$_2$,
(d) R^4 = H, or P(=O)(O-protecting group)$_2$,
(e) R^5 = H, or P(=O)(O-protecting group)$_2$,

(f) R^6 = H, P(=O)(O-protecting group)$_2$, , ω-aminoalkyl, ω-aminoalkenyl, ω-sulfhydrylalkyl, ω-carboxyalkyl, ω-(4-azidosalicylamido)-alkyl, alkyl-aminofluorophor, alkyl-amidofluorophor, or alkyl-fluorophor.

47. A selectively *O*-protected phosphoinositide analogue obtained as a phosphodiester intermediate formed by the reaction of a selectively protected *myo*-inositol phosphate or *scyllo*-inositol phosphate and an *sn*-3-phosphatidic acid or glycero ether analogue, wherein the said *O*-protected phosphoinositide analogue has the structure:



wherein at least one of R^3, R^4, R^5, R^6 is P(=O)(O-protecting group)$_2$,

and wherein

(a) X = F, Cl, Br, OC(=O)R, OR, or P(=O)(O-protecting group)$_2$, and Y = H; or X = Y = H; or

(b) X = H, and Y = F, Cl, Br, OC(=O)R, OR, or P(=O)(O-protecting group)$_2$, or

(c) X = Y = F or (=O);

where R = alkyl, especially methyl or ethyl, alkenyl, alkynyl, ω-aminoalkyl, N-substituted-ω-aminoalkyl or N,N-disubstituted-ω-aminoalkyl;

and wherein

(d) R^1 = RC(=O) or R, R^2 = R'C(=O) or R'

where R = alkyl, alkenyl, alkynyl, R' = ω-aminoalkyl, ω-(substitutedamino)-alkyl, ω-aminoalkenyl, ω-sulfhydrylalkyl, ω-carboxyalkyl, ω-(4-azidosalicylamido)-alkyl, ω-(substitutedamido)-alkyl, alkyl-aminofluorophor, alkyl-amidofluorophor, alkyl-fluorophor, hydroxylalkyl, or ketoalkyl; or where R' = alkyl, alkenyl, alkynyl, R = ω-aminoalkyl, ω-(substitutedamino)-alkyl, ω-aminoalkenyl, ω-sulfhydrylalkyl, ω-carboxyalkyl, ω-(4-azidosalicylamido)-alkyl,

ω-(substitutedamido)-alkyl, alkyl-aminofluorophor, alkyl-amidofluorophor, alkyl-fluorophor, hydroxylalkyl, or ketoalkyl; or where R = R';

and wherein

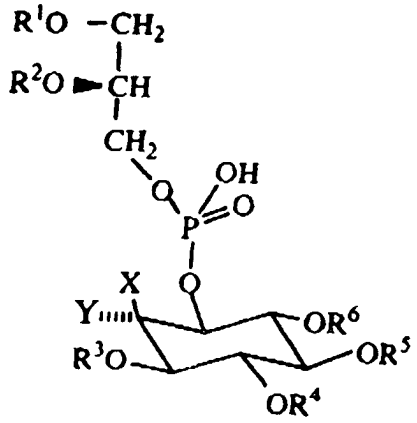
(e) R^3 = H, or P(=O)(O-protecting group)$_2$,

(f) R^4 = H, or P(=O)(O-protecting group)$_2$,

(g) R^5 = H, or P(=O)(O-protecting group)$_2$,

(h) R^6 = H, P(=O)(O-protecting group)$_2$, ω-aminoalkyl, ω-aminoalkenyl, ω-sulfhydrylalkyl, ω-carboxyalkyl, ω-(4-azidosalicylamido)-alkyl, alkyl-aminofluorophor, alkyl-amidofluorophor, or alkyl-fluorophor.

48. A phosphoinositide analogue based on phosphatidylinositolphosphate, wherein the 2-OH is rendered non-nucleophilic by derivatization or replacement or wherein a reporter group or conjugand is incorporated in the fatty acyl or inositol residue; wherein the core structure and absolute stereochemistry of the unmodified phosphatidylinositolphosphate is maintained in said phosphoinositide analogue; and wherein said phosphoinositide analogue has the structure:



wherein at least one of R^3, R^4, R^5, R^6 is P(=O)(OH)$_2$,

and wherein

(a) X = F, Cl, Br, OC(=O)R, OR, or OP(=O)(OH)$_2$, and Y = H; or
X = Y = H; or

(b) X = H, and Y = F, Cl, Br, OC(=O)R, OR, or OP(=O)(OH)$_2$; or

(c) X = Y = F or (=O);
where R = alkyl, especially methyl or ethyl, alkenyl, alkynyl, ω-aminoalkyl, N-substituted-ω-aminoalkyl or N,N-disubstituted-ω-aminoalkyl;

and wherein

(d) R^1 = RC(=O) or R, R^2 = R'C(=O) or R'
where R, R' = alkyl or alkenyl;

and wherein

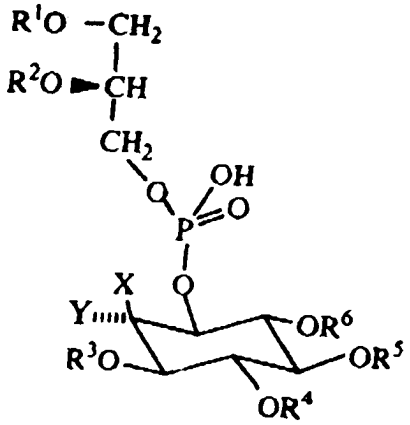
(e) R^3 = H, or $P(=O)(OH)_2$

(f) R^4 = H, or $P(=O)(OH)_2$

(g) R^5 = H, or $P(=O)(OH)_2$

(h) R^6 = H, $P(=O)(OH)_2$, ω-aminoalkyl, ω-aminoalkenyl, ω-sulfhydrylalkyl, ω-carboxyalkyl, ω-(4-azidosalicylamido)-alkyl, alkyl-aminofluorophor, alkyl-amidofluorophor, or alkyl-fluorophor.

49. A phosphoinositide analogue based on phosphatidylinositolphosphate, wherein the 2-OH is rendered non-nucleophilic by derivatization or replacement or wherein a reporter group or conjugand is incorporated in the fatty acyl or inositol residue; wherein the core structure and absolute stereochemistry of the unmodified phosphatidylinositolphosphate is maintained in said phosphoinositide analogue; and wherein said phosphoinositide analogue has the structure:



wherein at least one of R^3, R^4, R^5, R^6 is $P(=O)(OH)_2$,

and wherein

(a) X = OH, and Y = H; or X = H, and Y = OH;

and wherein

(b) R^1 = RC(=O) or R, R^2 = R'C(=O) or R'
where R = alkyl, alkenyl, alkynyl, R' = ω-aminoalkyl, ω-(substitutedamino)-alkyl, ω-aminoalkenyl, ω-sulfhydrylalkyl, ω-carboxyalkyl, ω-(4-azidosalicylamido)-alkyl, ω-(substitutedamido)-alkyl, alkyl-aminofluorophor, alkyl-amidofluorophor, alkyl-fluorophor, hydroxylalkyl, or ketoalkyl; or where R' = alkyl, alkenyl, alkynyl, R = ω-aminoalkyl, ω-(substitutedamino)-alkyl, ω-aminoalkenyl, ω-sulfhydrylalkyl, ω-carboxyalkyl, ω-(4-azidosalicylamido)-alkyl, ω-(substitutedamido)-alkyl, alkyl-aminofluorophor, alkyl-amidofluorophor, alkyl-fluorophor, hydroxylalkyl, or ketoalkyl; or where R = R', except when R = R' = alkyl;

and wherein

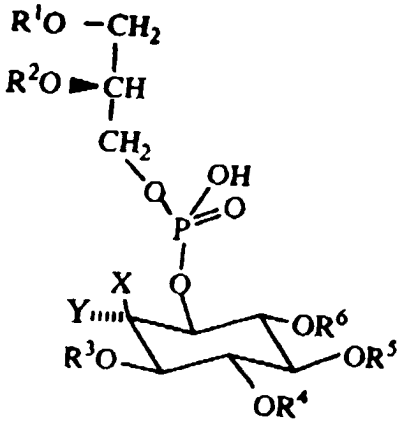
(c) R^3 = H, or $P(=O)(OH)_2$

(d) R^4 = H, or $P(=O)(OH)_2$

(e) R^5 = H, or $P(=O)(OH)_2$

(f) R^6 = H, $P(=O)(OH)_2$, ω-aminoalkyl, ω-aminoalkenyl, ω-sulfhydrylalkyl, ω-carboxyalkyl, ω-(4-azidosalicylamido)-alkyl, alkyl-aminofluorophor, alkyl-amidofluorophor, or alkyl-fluorophor.

50. A phosphoinositide analogue based on phosphatidylinositolphosphate, wherein the 2-OH is rendered non-nucleophilic by derivatization or replacement and a reporter group or conjugand is incorporated in the fatty acyl or inositol residue; wherein the core structure and absolute stereochemistry of the unmodified phosphatidylinositolphosphate is maintained in said phosphoinositide analogue; and wherein said phosphoinositide analogue has the structure:



wherein at least one of R^3, R^4, R^5, R^6 is $P(=O)(OH)_2$,

and wherein

(a) X = F, Cl, Br, OC(=O)R, OR, or $OP(=O)(OH)_2$, and Y = H; or
X = Y = H; or

(b) X = H, and Y = F, Cl, Br, OC(=O)R, OR, or $OP(=O)(OH)_2$; or

(c) X = Y = F or (=O);
where R = alkyl, especially methyl or ethyl, alkenyl, alkynyl, ω-aminoalkyl, N-substituted-ω-aminoalkyl or N,N-disubstituted-ω-aminoalkyl;

and wherein

(d) R^1 = RC(=O) or R, R^2 = R'C(=O) or R'
where R = alkyl, alkenyl, alkynyl, R' = ω-aminoalkyl, ω-(substitutedamino)-alkyl, ω-aminoalkenyl, ω-sulfhydrylalkyl, ω-carboxyalkyl, ω-(4-azidosalicylamido)-

alkyl, ω-(substitutedamido)-alkyl, alkyl-aminofluorophor, alkyl-amidofluorophor, alkyl-fluorophor, hydroxylalkyl, or ketoalkyl; or where R' = alkyl, alkenyl, alkynyl, R = ω-aminoalkyl, ω-(substitutedamino)-alkyl, ω-aminoalkenyl, ω-sulfhydrylalkyl, ω-carboxyalkyl, ω-(4-azidosalicylamido)-alkyl, ω-(substitutedamido)-alkyl, alkyl-aminofluorophor, alkyl-amidofluorophor, alkyl-fluorophor, hydroxylalkyl, or ketoalkyl; or where R = R';

and wherein

(e) R^3 = H, or $P(=O)(OH)_2$

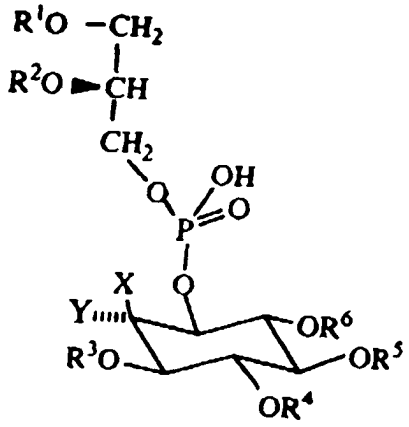
(f) R^4 = H, or $P(=O)(OH)_2$

(g) R^5 = H, or $P(=O)(OH)_2$

(h) R^6 = H, $P(=O)(OH)_2$, ω-aminoalkyl, ω-aminoalkenyl, ω-sulfhydrylalkyl, ω-carboxyalkyl, ω-(4-azidosalicylamido)-alkyl, alkyl-aminofluorophor, alkyl-amidofluorophor, or alkyl-fluorophor.

51. Matched pairs of the 2-modified phosphatidylinositol-phosphates of claim 48 and the corresponding phosphatidylinositol-phosphate structure lacking the 2-modification, wherein X=OH and Y=H, or X=H and Y=OH.

52. The phosphoinositide analogue of claim 11, wherein said phosphoinositide analogue has the structure:



wherein at least one of R^3, R^4, R^5, R^6 is $P(=O)(OH)_2$,

and wherein

(a) X = OH, and Y = H; or X = H, and Y = OH

and wherein

(b) R^1 = RC(=O) or R, R^2 = R'C(=O) or R'

where R = alkyl, alkenyl, alkynyl, R' = ω-aminoalkyl, ω-(substitutedamino)-alkyl, ω-aminoalkenyl, ω-sulfhydrylalkyl, ω-carboxyalkyl, ω-(4-azidosalicylamido)-alkyl, ω-(substitutedamido)-alkyl, alkyl-aminofluorophor, alkyl-amidofluorophor, [alkyl-fluorophor], hydroxylalkyl, or ketoalkyl; or where R' = alkyl, alkenyl, alkynyl, R = ω-aminoalkyl, ω-(substitutedamino)-alkyl, ω-aminoalkenyl, ω-sulfhydrylalkyl, ω-carboxyalkyl, ω-(4-azidosalicylamido)-alkyl, ω-(substitutedamido)-alkyl, alkyl-aminofluorophor, alkyl-amidofluorophor, hydroxylalkyl, or ketoalkyl;

and wherein

(c) R^3 = H, or $P(=O)(OH)_2$

(d) R^4 = H, or $P(=O)(OH)_2$

(e) R^5 = H, or $P(=O)(OH)_2$

(f) R^6 = H, $P(=O)(OH)_2$, ω-aminoalkyl, ω-aminoalkenyl, ω-sulfhydrylalkyl, ω-carboxyalkyl, ω-(4-azidosalicylamido)-alkyl, alkyl-aminofluorophor, alkyl-amidofluorophor, or alkyl-fluorophor.

53. A phosphoinositide analogue based on di-*O*-fattyacyl (or alkyl)-*sn*-glycero-3'-phospho-*myo*-inositol or di-*O*-fattyacyl (or alkyl)-*sn*-glycero-3'-phospho-*scyllo*-inositol having at least one additional hydroxyl group derivatized as a phosphate, wherein said phosphoinositide analogue incorporates one or more of the following modifying structural features:

(a) the 2-OH is rendered non-nucleophilic by derivatization or replacement; or

(b) a conjugand suitable for linking to a reporter group, polymer, chromatographic matrix, or gold surface is incorporated in the fattyacyl or inositol residue; wherein said conjugand is selected from the group consisting of ω-aminoalkyl, ω-(substitutedamino)-alkyl, ω-aminoalkenyl, ω-sulfhydrylalkyl, ω-carboxyalkyl, hydroxylalkyl and ketoalkyl, and wherein the amino, substitutedamino, sulfhydryl, carboxyl, hydroxyl and keto functions are free and unsubstituted, or are covalently linked to a reporter group;

wherein the core structure and absolute stereochemistry of the unmodified di-*O*-fattyacyl (or alkyl)-*sn*-glycero-3'-phospho-*myo*-inositol phosphate or di-*O*-fattyacyl (or alkyl)-*sn*-glycero-3'-phospho-*scyllo*-inositol phosphate is maintained in said phosphoinositide analogue.

EXHIBIT C
EXPLANATION OF AMENDMENTS
WITH REFERENCE TO SERIAL NO.08/872,222

The following explanations of the changes in the substitute specification are made with reference to the text of Application Serial No. 08/872,222 as originally filed.

At page 1, line 3 of the text, before "This invention was", the inserted text reads -- The present application claims priority to co-pending application Serial No. 08/872,222, filed June 10, 1997; which claims priority to provisional application Serial No. 60/019,651, filed June 11, 1996. --.

At page 6, line 22 of the text, the deleted text reads "themajor" and the inserted text reads -- the major --.

At page 10, line 23 of the text, in the center of the page, the deleted text reads "methoxybenzyl)-*myo*-inositol" and the inserted text reads -- methoxybenzyl)-*myo/scyllo*-inositol --.

At page 11, lines 5, 11, 13, 19, 23 and bridging lines 25 and 26 of the text, each instance of the deleted text reads "-*myo*-inositol" and each instance of the inserted text reads -- -*myo/scyllo*-inositol --.

At page 12, line 10 of the text, the deleted text reads "-*myo*-inositol" and the inserted text reads -- -*myo/scyllo*-inositol --.

At page 12, lines 15 and 24 of the text, in the center of the page, each instance of the deleted text reads "-*scyllo*-inositol" and each instance of the inserted text reads -- -*myo/scyllo*-inositol --.

At page 12, line 18 of the text, the deleted text reads "*myo*-inositol" and the inserted text reads -- *myo/scyllo*-inositol --.

At page 13, line 2 of the text, the deleted text reads "-*myo*-inositol" and the inserted text reads -- -*myo/scyllo*-inositol --.

At page 13, lines 3 and 20 of the text, each instance of the deleted text reads "-*scyllo*-inositol" and each instance of the inserted text reads -- -*myo/scyllo*-inositol --.

At page 14, lines 6, 8 and 11 of the text, in the center of the page, each instance of the deleted text reads "-*myo*-inositol" and each instance of the inserted text reads -- -*myo/scyllo*-inositol --.

At page 14, line 18 of the text, the deleted text reads "1D-3,6-Di-*O*-benzyl-4,5-di-*O*-cyclohexylidene-1-(*p*-methoxybenzyl)-*myo*-inositol" and the inserted text reads -- 1D-3,6-Di-*O*-benzyl-4,5-*O*-cyclohexylidene-1-(*p*-methoxybenzyl)-*myo*-inositol --.

Exhibit D

Searching 1999-2000...

Results of Search in 1999-2000 db for:
"reporter group" OR "reporter molecule": 790 patents.
Hits 1 through 50 out of 790

Next 50 Hits | Jump To | Refine Search | "reporter group" OR "reporter molecule"

	PAT. NO.	Title
1	6,114,517	Methods of modulating tumor necrosis factor .alpha.-induced expression of cell adhesion molecules
2	6,114,513	Thiol-derivatized oligonucleotides
3	6,114,350	Cyanine dyes and synthesis methods thereof
4	6,114,177	Fluorometric assay for measurement of antioxidant activity
5	6,114,160	Compositions and methods for taxol biosynthesis
6	6,114,117	Homogeneous diagnostic assay method utilizing simultaneous target and signal amplification
7	6,113,904	Human glycoprotein
8	6,111,094	Enhanced antisense modulation of ICAM-1
9	6,111,085	Carbamate-derivatized nucleosides and oligonucleosides
10	6,110,747	Compounds and methods for modulating tissue permeability
11	6,110,722	F.sub.0 ATP synthase subunit
12	6,110,693	Methods of assaying receptor activity and constructs useful in such methods
13	6,110,687	Detection of antigens via oligonucleotide antibody conjugates
14	6,110,686	DNA hybridizing to a human cystatin-like protein (CSTIN)
15	6,110,682	Signal enhancement method and kit
16	6,110,677	Oligonucleotide modification, signal amplification, and nucleic acid detection by target-catalyzed product formation
17	6,110,675	Reagents and methods useful for detecting diseases of the prostate
18	6,110,664	Antisense inhibition of G-alpha-S1 expression
19	6,110,630	Efficient activated cyanine dyes
20	6,110,507	Human 3-hydroxyisobutryl-coenzyme a hydrolase
21	6,107,472	Receptor-type tyrosine kinase-like molecules
22	6,107,283	Cardiac glycosides inhibit proliferation of cells bearing FGF receptors

23 6,107,092 Antisense modulation of SRA expression
24 6,107,091 Antisense inhibition of G-alpha-16 expression
25 6,107,039 Assays using base protected table 1
26 6,106,844 Immunomodulatory peptides of vespid antigen 5
27 6,106,732 Integral blood plasma or serum isolation, metering and transport device
28 6,103,877 Tumor suppressor gene, HIC-1
29 6,103,874 Human KDEL receptor
30 6,103,537 Capillary assays involving separation of free and bound species
31 6,103,497 Human S100 proteins
32 6,103,483 Molecule involved in binding of sperm to egg surfaces and procedures for use of this molecule to enhance or decrease potential fertility
33 6,103,479 Miniaturized cell array methods and apparatus for cell-based screening
34 6,103,477 Rho protein
35 6,103,474 Hybridization assay signal enhancement
36 6,103,469 Human phospholipase A2 protein
37 6,103,217 Polymeric assemblies for sensitive colorimetric assays
38 6,103,199 Capillary electroflow apparatus and method
39 6,100,090 Antisense inhibition of PI3K p85 expression
40 6,100,075 Delta 1-pyrroline-5-carboxylate reductase homolog
41 6,100,048 Methods and reagents for discovering and using mammalian melanocortin receptor agonists and antagonists to modulate feeding behavior in animals
42 6,100,040 Methods and compositions for detection of specific nucleotide sequences
43 6,100,037 Human cyclic nucleotide PDEs
44 6,100,036 NADH dehydrogenase B17 subunit
45 6,100,034 Detection of retroviral subtypes based upon envelope specific sequences
46 6,100,027 Nucleic acid probes and amplification oligonucleotides for Neisseria species
47 6,100,024 Methods and compositions for nucleic acid detection by target extension and probe amplification
48 6,099,803 Advanced active electronic devices for molecular biological analysis and diagnostics
49 6,096,725 Methods of using .alpha.Gal oligosaccharides as immune system targeting agents
50 6,096,722 Antisense modulation of cell adhesion molecule expression and treatment of cell adhesion molecule-associated diseases

Searching 1999-2000...

Results of Search in 1999-2000 db for:
"reporter group" OR "reporter molecule": 790 patents.
Hits 51 through 100 out of 790

Prev 50 Hits
Next 50 Hits
Jump To
Refine Search "reporter group" OR "reporter molecule"

	PAT. NO.	Title
51	6,096,720	Liposomal oligonucleotide compositions
52	6,096,543	Antisense inhibition of human mek1 expression
53	6,096,502	Substrate for detecting UL9 helicase activity
54	6,096,308	Human protein kinase and kinase inhibitors
55	6,093,811	Oligonucleotide modulation of cell adhesion
56	6,093,809	Telomerase
57	6,093,565	Protein phosphatase regulatory subunit
58	6,093,538	Nucleic acid probes to ureaplasma
59	6,093,537	Double receptor polynucleotide assay method
60	6,091,003	Compositions and methods for genetic transformation of pineapple
61	6,090,786	Serine proteases, their activity and their synthetic inhibitors
62	6,090,631	Methods and compositions for screening for presynaptic calcium channel blockers
63	6,090,626	Antisense oligonucleotide modulation of raf gene expression
64	6,090,620	Genes and gene products related to Werner's syndrome
65	6,090,606	Cleavage agents
66	6,090,591	Selective amplification of target polynucleotide sequences
67	6,090,589	Nucleic acid amplification with DNA-dependent RNA polymerase activity of RNA replicases
68	6,090,578	MTS1 gene
69	6,090,577	Disease associated acidic protein
70	6,090,564	SnRNP Sm proteins
71	6,090,543	Cleavage of nucleic acids
72	6,090,390	Diagnostic test for equine arteritis virus mediated disease

73 6,090,386 T cell peptides of the CRX JII allergen
74 6,090,377 Monocyte activating cytokine
75 6,087,489 Antisense oligonucleotide modulation of human thymidylate synthase expression
76 6,087,486 Nucleotide sequences encoding vpr receptor protein
77 6,087,333 Disease associated acidic protein
78 6,087,178 Method for down regulating CD4 expression in a T cell
79 6,087,173 Antisense modulation of X-linked inhibitor of apoptosis expression
80 6,087,172 Ribozymes targeted to human IL-15 mRNA
81 6,087,125 Polynucleotide encoding a novel human nm23-like protein
82 6,087,108 RNA editing enzyme
83 6,084,102 Covalently linked oligonucleotide minor grove binder conjugates
84 6,084,082 Lactam nucleic acids
85 6,084,070 Human glutaredoxin .beta.
86 6,083,929 Extended type 1 chain glycosphingolipids as tumor-associated antigens
87 6,083,923 Liposomal oligonucleotide compositions for modulating RAS gene expression
88 6,083,758 Method for screening peptides for metal coordinating properties and fluorescent chemosensors derived therefrom
89 6,083,750 Adenovirus vectors
90 6,083,724 Recombinant avian interferon-gamma (IFN-.gamma.)
91 6,083,706 Inhibitors of leaderless protein export
92 6,083,704 Human cytochrome b5
93 6,083,689 Sensitive immunoassays utilizing antibody conjugates with replicable DNA templates
94 6,080,868 Nitro-substituted non-fluorescent asymmetric cyanine dye compounds
95 6,080,848 Human brain associated protein
96 6,080,847 Proteins associated with cell proliferation
97 6,080,842 Human ATP binding-cassette transport protein
98 6,080,841 Human induced tumor protein
99 6,080,723 Human actVA-ORF4-like protein
100 6,080,558 Polynucleotide encoding human growth regulator protein

Exhibit E

US006093538A

United States Patent [19]

Hogan et al.

[11] **Patent Number: 6,093,538**

[45] **Date of Patent: Jul. 25, 2000**

[54] **NUCLEIC ACID PROBES TO UREAPLASMA**

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[21] Appl. No.: **08/109,037**

[22] Filed: **Aug. 18, 1993**

Related U.S. Application Data

[63] Continuation-in-part of application No. 07/879,686, May 6, 1992, abandoned.

[51] **Int. Cl.**[7] **C12Q 1/68**; C07H 21/04

[52] **U.S. Cl.** **435/6**; 536/24.32; 536/24.33; 536/23.1

[58] **Field of Search** 435/6; 536/24.32, 536/24.33, 23.1; 935/878; 514/44

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Attorney, Agent, or Firm—Brobeck, Phleger & Harrison

[57] **ABSTRACT**

Hybridization assay probes are described which are able to distinguish Ureaplasma and known strains or serotypes of the species *Ureaplasma urealyticum* found in humans from other related organisms.

107 Claims, No Drawings

NUCLEIC ACID PROBES TO UREAPLASMA

This application is a continuation-in-part of Kacian et al., entitled "Nucleic Acid Sequence Amplification Method, Composition and Kit," U.S. Ser. No. 07/879,686 filed May 6, 1992, now abandoned hereby incorporated by reference herein.

FIELD OF THE INVENTION

The invention described and claimed herein relates to the design and use of nucleic acid probes capable of detecting organisms of the genus Ureaplasma, and known strains or serotypes of the species Ureaplasma urealyticum, in test samples, e.g., from urogenital and endocervical specimens, tissue samples, amniotic and other body fluids, and from cultures.

BACKGROUND OF THE INVENTION

Two single strands of deoxyribo- ("DNA") or ribo- ("RNA") nucleic acid, formed from nucleotides, (including the bases adenine (A), cytosine (C), thymidine (T), guanine (G), uracil (U), or inosine (I)), may hybridize to form a double-stranded structure held together by hydrogen bonds between pairs of complementary bases. Generally, A is hydrogen bonded to T or U, while G or I are hydrogen bonded to C. Along the chain, classical base pairs AT or AU, TA or UA, GC, or CG are present. Additionally, some mismatched base pairs (e.g., AG, GU) may be present.

Bringing together two single strands of nucleic acid containing sufficient contiguous complementary bases, under conditions which will promote their hybridization, results in double-stranded nucleic acid. Under appropriate conditions, DNA/DNA, RNA/DNA, or RNA/RNA hybrids can form.

A probe is generally a single-stranded nucleic acid sequence complementary to some degree to a nucleic acid sequence sought to be detected ("target sequence"). A probe may be labeled with a reporter group moiety such as a radioisotope, a fluorescent or chemiluminescent moiety, or with an enzyme or other ligand which can be used for detection. Background descriptions of the use of nucleic acid hybridization to detect particular nucleic acid sequences are given in Kohne, U.S. Pat. No. 4,851,330 issued Jul. 25, 1989, and by Hogan et al., International Patent Application No. PCT/US87/03009, entitled "Nucleic Acid Probes for Detection and/or Quantitation of Non-Viral Organisms," both references hereby incorporated by reference herein. Hogan et al., supra, describe methods for determining the presence of a non-viral organism or a group of non-viral organisms in a sample (e.g., sputum, urine, blood and tissue sections, food, soil and water).

The genera Ureaplasma and Mycoplasma are prokaryotes and comprise the taxonomic Mollicutes class. Mollicutes lack a bacterial cell wall and have a small genome size. They are considered one of the smallest of the free-living micro-organisms. Ureaplasma are unique among Mollicutes because of their characteristic ability to metabolize urea. There are fourteen known serotypes of *U. urealyticum* (Stemke and Robertson, *Diagn. Microbiol. Infect. Dis.* 31: 311 (1985)). The fourteen serotypes can be divided into at least two subspecies ("biotypes") based upon restriction fragment length polymorphism ("RFLP") of *U. urealyticum* genomic DNA (Harasawa et al., *Abstract S30-6 UIMS Meeting,* Osaka Japan (1990), and Robertson et al., *J. Clin. Microbiol.* 31: 824 (1993)), or based upon rRNA sequences (Hammond et al., *Abstract D17. Session 60, American Society for Microbiology General Meeting,* (1991)).

U. urealyticum is commonly found in the human urogenital tract but has been implicated in a wide spectrum of pathologies. Several studies have implicated *U. urealyticum* as a possible etiologic agent in diseases affecting adult males, fetuses and infants. Brunner et al., *Yale J. Biol. Med.* 56: 545 (1983), identified *U. urealyticum* as the etiologic agent responsible for nongonococcal urethritis (NGU) in approximately 30 percent of adult males tested who had NGU. Cassell et al., *Pediatr. Infect. Dis.* 5: S247 (1986), implicated *U. urealyticum* as a possible cause of chorioamnionitis, which could in turn adversely affect the outcome of pregnancy and the health of neonates. Stagno et al., *Pediatrics* 68: 322 (1981), found *U. urealyticum* in 21% of infants with pneumonia and found the association of *U. urealyticum* with pneumonia to be "statistically significant." Waites et al., *Lancet* 8575: 17 (1988), found *U. urealyticum* in 8 percent of the cerebrospinal fluid specimens taken from a high-risk population of newborn infants (100 predominantly pre-term infants). According to these investigators *U. urealyticum* was the most common organism isolated of those sought. *U. urealyticum* has also been implicated in a number of other pathogenic states including septic arthritis (Lee et al., *Arthritis and Rheumatism* 35: 43 (1992)).

Standard microbiological techniques generally identify *U. urealyticum* by observing the hydrolysis of urea. These techniques usually involve inoculating both a complex broth medium and an agar medium containing urea and other nutrients with a freshly obtained specimen (Brunner et al., supra).

References concerning detection of Ureaplasma include the following: Roberts et al., *Israel J. Med. Sci.,* 23: 618 (1987), describe the use of whole chromosomal DNA probes for detection of Ureaplasma in genital specimens; Ohse and Göbel, *Israel J. Med. Sci.* 23: 352 (1987) describe hybridization of *U. urealyticum* rRNA genes to cloned DNA of the *E. coli* rRNA operon; Gobel and Stanbridge ("Detection of Mycoplasma by DNA Hybridization", EPO application number 86304919.3, publication number 0 250 662) mention biological probes for detecting Mycoplasmas or prokaryotes in general, or specific Mycoplasma and eubacterial species; Gonzales et al. (*American Society for Microbiology Annual Meeting* 1991, *Abstract D*-16) mentions a method to detect Ureaplasma using a DNA probe directed to rRNA; Lee et al., supra, and Willoughby et al., *Infection and Immunity* 59: 2463 (1991), describe a procedure for detecting the *U. urealyticum* urease gene utilizing PCR; Deng et al., *PCR Methods and Applications* 1: 202 (1992), suggest that PCR-RFLP techniques should be capable of detecting Mollicutes; Brogan et al., *Molecular and Cellular Probes* 6: 411 (1992), describe the amplification of a 186 base pair genomic *U. urealyticum* DNA fragment; Robertson et al., supra, describe a technique involving the polymerase chain reaction using biotype specific primers to 16S rRNA gene sequences to distinguish the two *U. urealyticum* biotypes.

SUMMARY OF THE INVENTION

The featured invention discloses and claims novel oligonucleotide probes which are either targeted to a specific Ureaplasma nucleic acid target sequence or consist essentially of a specified nucleic acid sequence. The probes function by hybridizing to target *U. urealyticum* rRNA and/or rRNA gene sequences under stringent hybridization assay conditions. Thus, the probes can distinguish the genus Ureaplasma, including clinically significant *U. urealyticum* serotypes, from their known closest phylogenetic neighbors (Mycoplasma) and from other microorganism inhabitants of the human urogenital tract. Accordingly, the probes may be

used in an assay to detect and/or quantitate Ureaplasma and *U. urealyticum* organisms.

Species of Mycoplasma found in humans include *M. genitalium, M. pneumoniae* and *M. hominis. M. pneumoniae* appears to be the most closely related Mycoplasma to *U. urealyticum. M. genitalium* is very similar in nucleic acid sequence to *M. pneumoniae* and has been isolated from the human genital tract. *M. hominis* is the most commonly isolated Mycoplasma from the genital tract.

Thus, in a first aspect, the invention described herein features hybridization assay probes able to selectively hybridize to a Ureaplasma target nucleic acid sequence. A Ureaplasma target nucleic acid sequence is a nucleic acid sequence present in Ureaplasma, preferably *U. urealyticum* nucleic acid, or a sequence complementary thereto. Preferably, the target nucleic acid sequence is not present in closely related Mycoplasma (e.g., *M. pneumoniae*). Sequences complementary to a target sequence may be generated by target amplification techniques such as polymerase chain reaction (PCR) or transcription mediated amplification (e.g., Kacian and Fultz, entitled "Nucleic Acid Amplification Methods", EPO application number 90307503.4; and Kacian et al., supra entitled "Nucleic Acid Sequence Amplification Method, Composition and Kit."

The featured probes can detect *U. urealyticum* and distinguish the genus Ureaplasma and known strains or serotypes of *U. urealyticum* found in humans from other bacteria including the phylogenetic closely related *M. pneumoniae.*

A hybridization assay probe is comprised of an oligonucleotide having a nucleic acid sequence sufficiently complementary to hybridize, under stringent hybridization assay conditions, to a 5S, 16S, or 23S rRNA, or to the corresponding ribosomal DNA ("rDNA") nucleic acid sequence, or to a nucleic acid sequence complementary thereto, of *U. urealyticum.* Stringent hybridization assay conditions, refer to conditions wherein a specific probe hybridizes with target nucleic acid (e.g., rRNA of Ureaplasma) and not another nucleic acid present in the test sample from either other microorganisms (e.g., *Mycoplasma pneumonia*) or humans. The probes are preferably 10 to 100 nucleotides in length.

By "probe" is meant to exclude naturally occurring nucleic acids. Purified oligonucleotide probes may be produced by techniques known in the art such as chemical synthesis and by in vitro or in vivo expression from recombinant nucleic acid molecules, e.g., retroviral vectors.

An oligonucleotide is made of nucleotide subunits covalently joined together. The sugar groups of the nucleotide subunits may be ribose, deoxyribose, or modified derivatives thereof such as O-methyl ribose. The nucleotide subunits may by joined by linkages such as phosphodiester linkages, modified linkages, or by non-nucleotide moieties that do not prevent hybridization of the oligonucleotide. Modified linkages include those linkages in which a standard phosphodiester linkage is replaced with a different linkage, such as a phosphorothioate linkage, or methylphosphonate linkage. When used as a hybridization assay probe, the oligonucleotide preferably contains a reporter group such as acridinium ester or a radioisotope to help identify hybridization of the probe to its target sequence.

In a related aspect, the invention described herein features hybridization assay probes able to selectively hybridize to a *U. urealyticum* nucleic acid target sequence present on either biotype 1 or biotype 2. The claimed target sequence is present in only one of the biotypes. Thus, an oligonucleotide probe directed to either biotype 1 or biotype 2 target site can distinguish between the biotypes.

In another related aspect, hybridization assay probes having a specific nucleic acid sequences complementary to rRNA or rDNA of Ureaplasma, are described. The probes are useful for detecting and/or quantitating Ureaplasma which may be present. These probes are complementary to a region of rRNA or rDNA which varies between Ureaplasma and Mycoplasma. Specific probes able to hybridize to Ureaplasma nucleic acid and distinguish Ureaplasma from Mycoplasma, comprise, consist essentially of, or consist of the sequences (written 5' to 3'):

(SEQ ID NO: 2) ACCTCTCAGT ACAGCTACGC G

(SEQ ID NO: 5) CATTTCCTAT CTTAGCGTTT CTTCCC

(SEQ ID NO: 8) CGTTAAGCAT CTAGATTTAA TACCAAACTT ACAAACCCG

(SEQ ID NO: 9) CCTACTACAC TCTAGGTTTA CAGTTTTTGA TACAGCTAGA

(SEQ ID NO: 11) GTCAGTGATA GTCCAAGTTG GC

(SEQ ID NO: 14) CGTTCGAGCC GACATTTAAT GATGATCG

(SEQ ID NO: 17) GCGTCGCAAT AGATGTCAAA CCTAG

(SEQ ID NO: 20) CGATTTTGCA GCAGTTTGTA TTAGCCATTG

(SEQ ID NO: 22) GCTATTTTCG GCTCTAGAGT GCTTGACTTC TGTGTTCGGG ATG

(SEQ ID NO: 23) CGGCTCTAGA GTGCTTGACT TCTGTGTTCG

(SEQ ID NO: 26) GGATGGGAAC AGGTATTTCC ACTCTGATAT GATCAC

(SEQ ID NO: 29) CAGTAATCTA ATTCTCATTA GACTGAGTTT CCTCATTCG and RNA equivalents thereto (SEQ ID NOs: 31, 34, 37, 40, 43, 46, 49, 52, 55, 58, 61, and 109), oligonucleotides complementary thereto (SEQ ID NOs: 32, 35, 38, 41, 44, 47, 50, 53, 56, 59, 62 and 110), and RNA equivalents to the oligonucleotides complementary thereto (SEQ ID NOs: 33, 36, 39, 42, 45, 48, 51, 54, 57, 60, 63, 111). Preferably, helper probe are used to facilitate the hybridization of the assay probe to its target nucleic acid sequence.

The phrases "consists essentially of" or "consisting essentially of" mean that the probe is provided as an oligonucleotide which hybridizes under stringent hybridization assay conditions to a target nucleic acid sequence of a particular organism and preferably does not hybridize with Mycoplasma described herein. A hybridization probe may be linked to other nucleic acids which do not affect hybridization. Generally, it is preferred that the probe be between 10 and 100 (most preferably between 15 and 50) nucleotides in length. Additionally, the probe may be provided in a vector.

For the listed probes, two sets of stringent hybridization assay conditions were used. One set comprised hybridization at 60° C. for one hour in a solution containing 0.095 M lithium succinate pH 5, 0.31 M lithium lauryl sulfate, 1.5 mM ethylenediaminetetraacetic acid (EDTA), 1.5 mM ethylene glycol bis (beta-amino ethyl ether) N, N, N', N' tetraacetic acid (EGTA). After the one hour, hybrids were separated from unhybridized probe by binding to magnetic amine microspheres in a solution containing 0.76 M sodium borate pH 7.5, 6% Triton at 60° C. for ten minutes and washed once in a solution containing 80 mM sodium borate pH 10.4 at room temperature.

Another set of stringent hybridization assay conditions was comprised of hybridization in 0.05 M lithium succinate pH 5, 0.6 M LiCl, 1% (w/v) lithium lauryl sulfate, 10 mM EDTA, 10 mM EGTA at 60° C. for 15 minutes, followed by the addition of 300 μl of 0.6 M sodium borate pH 8.5, 1% Triton X-100 at 60° C. for 5–7 minutes. Additional sets of

stringent hybridization conditions can be determined based upon techniques known in the art and the present disclosure.

In another aspect, specific probes able to distinguish between different biotypes are described. Specific probes able to hybridize to a nucleic acid sequence present in only one Ureaplasma biotype comprise, consist essentially of, or consist of the sequences (written 5' to 3'):

SEQ ID NO. 121: CAACACCGAC TCGTTCGAGC

SEQ ID NO. 122: CAACACCGAC CCATTCGG and RNA equivalents thereto (SEQ ID NOs: 126 and 127), oligonucleotides complementary thereto (SEQ ID NOs: 131 and 132), and RNA equivalents to the oligonucleotides complementary thereto (SEQ ID NOs: 136 and 137). Preferably, a helper probe is used to facilitate the hybridization of the assay probe to its target nucleic acid sequence.

In another aspect, specific helper probe oligonucleotide sequences have been determined. Helper probes are used to facilitate the rate of hybridization of a hybridization assay probe to its target nucleic acid as described by Hogan and Milliman, U.S. Pat. No. 5,030,557 entitled "Means and Method for Enhancing Nucleic Acid Hybridization," issued Jul. 9, 1991 and hereby incorporated by reference herein. Helper probes featured herein include: SEQ ID NOs. 1, 3, 4, 6, 7, 8, 9, 10, 12, 13, 15, 16, 18, 19, 21, 24, 25, 26, 27, 28, 30, 123, 124, 125; RNA equivalents thereto, SEQ ID NOs. 37, 40, 64, 67, 70, 73, 76, 79, 82, 85, 88, 91, 94, 97, 100, 103, 106, 109, 112, 115, 118, 128, 129, 130; oligonucleotides complementary thereto, SEQ ID NOs. 38, 41, 65, 68, 71, 74, 77, 80, 83, 86, 89, 92, 95, 98, 101, 104, 107, 110, 113, 116, 119, 133, 134, 135; and RNA equivalents to the oligonucleotides complementary thereto, SEQ ID Nos. 39, 42, 66, 69, 72, 75, 78, 81, 84, 87, 90, 93, 96, 99, 102, 105, 108, 111, 114, 117, 120, 138, 139, 140.

Some oligonucleotide probes can be used as an assay probe or a helper probe (e.g., SEQ ID Nos. 8, 9, and 26, RNA equivalents thereto, SEQ ID Nos. 37, 40, and 109, oligonucleotides complementary thereto, 38, 41, and 110, and RNA equivalents to the oligonucleotides complementary thereto 39, 42, and 111.

In another related aspect, the invention features compositions comprising a nucleic acid hybrid between a hybridization assay probe and a nucleic acid sequence substantially complementary thereto (probe:target). "Substantially complementary" means there is sufficient complementarity between the nucleic acids such that the hybrid is stable under stringent hybridization conditions. One use of the formed hybrid is to detect the presence of a target sequence. For example, acridinium ester ("AE") present in hybrids is resistant to hydrolysis in alkali solution whereas acridinium ester present in single-stranded nucleic acid is hydrolyzed in alkali solution (Arnold et al., entitled "Homogeneous Protection Assay," EPO application number 88308767.8, publication number 309230, hereby incorporated by reference herein). Thus, binding of AE-labeled probe to target can be detected, after hydrolysis of the unbound AE-labeled probe, by measuring chemiluminescence of acridinium ester remaining in the nucleic acid hybrid.

In other related aspects, methods are described for detecting *Ureaplasma urealyticum* and distinguishing *Ureaplasma urealyticum* from Mycoplasma such as *Mycoplasma orale, Mycoplasma fermentans, Mycoplasma capricolum, Mycoplasma lipophilum,* and *Mycoplasma salivarium;* distinguishing between *Ureaplasma urealyticum* biotype 1 and *Ureaplasma urealyticum* biotype 2; and detecting the presence of a *Ureaplasma urealyticum* nucleic acid sequence. These methods can be used on test samples obtained from human specimens.

The probes of this invention offer a rapid, non-subjective method of identifying and quantitating the presence of specific rRNA sequences unique to the genus Ureaplasma and all strains of *U. urealyticum* in a test sample.

Other features and advantages of the invention will be apparent from the following description of the preferred embodiments thereof and from the claims.

DESCRIPTION OF THE PREFERRED EMBODIMENTS

We have identified preferred target sequences present in the rRNA or rDNA of *U. urealyticum* and designed specific oligonucleotide probes to these sequences and their complements which can be used to identify Ureaplasma. The probes can detect the genus Ureaplasma including *U. urealyticum* serotypes and distinguish them from their known and presumably most closely related taxonomic or phylogenetic neighbors. Probes are also described which distinguish *U. urealyticum* biotype 1 and biotype 2. Also described are methods using the featured probes or target sites.

In a preferred embodiment, the nucleic acid hybridization assay probes can distinguish *U. urealyticum* from *M. genitalium, M. pneumoniae,* or *M. hominis.* In another preferred embodiment, the nucleic acid hybridization probes can distinguish *U. urealyticum* from *M. orale, M. fermentans, M. capricolum, M. lipophilum,* and *M. salivarium.* These Mycoplasma have been isolated from humans.

Prokaryotic organisms (excluding viruses) contain rRNA genes encoding 5S rRNA, 16S rRNA and 23S rRNA. Using methods known to those skilled in the art, partial or full rRNA sequences of *U. urealyticum* and Mycoplasma were obtained. These sequences were aligned based on regions of sequence homology. Sequence variations were then identified from the aligned sequences and used as target sequences for hybridization assay probes.

Obtaining rRNA Sequences

Sequence information was obtained experimentally and from published information (see, Weisburg et al., *J. Bacteriol* 171: 6455 (1989); and Rogers et al., Proc. Natl. Acad. Sci., U.S.A., 82: 1160 (1985)). Experimental information was obtained by isolating and sequencing the ribonucleic acid from various organisms using sequence standard techniques known in the art. Nucleic acids were obtained using an oligonucleotide primer complementary to a conserved region of rRNA and extending the primer using reverse transcriptase. Nucleic acid sequences were then derived using the method of dideoxynucleotide chain termination. (e.g., Lane et al., *Proc. Natl. Acad. Sci. U.S.A.,* 82: 6955 (1985)).

Probe Design And Hybridization Conditions

To facilitate the identification of nucleic acid sequences to be used as probes, the nucleotide sequences from different organisms were first aligned to maximize homology. Within the rRNA molecule there is a close relationship between secondary structure and function. This imposes restrictions on evolutionary changes in the primary sequence so that the secondary structure is maintained. For example, if a base is changed on one side of a helix, a compensating change is made on the other side to preserve the complementarity (this is referred to as co-variance). This allows two very different sequences to be aligned based on the conserved primary sequence and also on the conserved secondary structure elements. Potential target sequences for the hybridization probes were identified by noting variations in the homology of the aligned sequences.

The sequence evolution at each of the variable regions is mostly divergent. Because of the divergence, more distant

phylogenetic relatives of *U. urealyticum* show greater variability to *U. urealyticum* at the variable region than phylogenetically closer relatives. We observed sufficient variation between *U. urealyticum* and strains of Mycoplasma found in the same sample to design several useful probes and identify preferred target sites.

Selective hybridization of probe to target can be accomplished by choosing the appropriate hybridization assay conditions and proper probe design. The stability of the probe:target nucleic acid hybrid should be chosen to be compatible with the assay and washing conditions so that hybrids will only form between highly complementary sequences. Manipulation of one or more of the different assay conditions determines the exact sensitivity and specificity of a particular probe. The following guidelines are useful for designing probes and determining stringent hybridization assay conditions.

Probes should be designed to have an appropriate melting temperature (T_m). The appropriate T_m can be obtained by varying the probe length and nucleotide composition (percentage of G+C versus A+T). The probe length and nucleotide composition should preferably be chosen to correspond to a T_m about 2–10° C. higher than the temperature at which the final assay will be performed.

In general, the optimal hybridization temperature for oligonucleotide probes of about 10–50 bases in length is approximately 5° C. below the melting temperature for a given duplex. Incubation at temperatures below the optimum temperature may allow mismatched base sequences to hybridize and can therefore decrease specificity. The longer the probe, the more hydrogen bonding between base pairs and, in general, the higher the T_m. Increasing the percentage of G and C also increases the T_m because G-C base pairs exhibit additional hydrogen bonding and therefore greater thermal stability than A-T base pairs.

The preferred method to determine T_m measures hybridization using a Hybridization Protection Assay (HPA) according to Arnold et al., supra entitled "Homogeneous Protection Assay." T_m can be measured using HPA in the following manner. A probe:target hybrid is formed in a lithium succinate buffered solution (0.1 M lithium succinate buffer, pH 5.0, 2 mM EDTA, 2 mM EGTA, 10% (w/v) lithium lauryl sulfate) using an excess amount of target. Aliquots of the hybrid are then diluted in the lithium succinate buffered solution and incubated for five minutes at various temperatures starting below that of the anticipated T_m (typically 55° C.) and increasing in 2–5° C. increments. This solution is then diluted with a mild alkaline borate buffer (0.15 M sodium tetraborate, pH 7.6, 5% (v/v) Triton X-100)) and incubated at a lower temperature (for example 50° C.) for ten minutes. Under these conditions the acridinium ester attached to a single-stranded probe is hydrolyzed while the acridinium ester attached to hybridized probe is relatively protected from hydrolysis. Thus, the amount of acridinium ester remaining is proportional to the amount of hybrid and can be measured by the chemiluminescence produced from the acridinium ester upon the addition of hydrogen peroxide followed by alkali. Chemiluminescence can be measured in a luminometer (e.g., the Gen-Probe LEADER I or LEADER 50). The resulting data is plotted as percent of maximum signal (usually from the lowest temperature) versus temperature. The T_m is defined as the temperature at which 50% of the maximum signal remains. In addition to the method above, T_m may be determined by isotopic methods well known to those skilled in the art (e.g., Hogan et al., supra).

It should be noted that the T_m for a given hybrid varies depending on the hybridization solution used. Factors such as the salt concentration, detergents, and other solutes can affect hybrid stability during thermal denaturation (J. Sambrook, E. F. Fritsch and T. Maniatis, *Molecular Cloning*, ch. 11 (2d ed. 1989)). Conditions such as ionic strength and incubation temperature under which a probe will be used to hybridize to target should be taken into account in constructing a probe. Thermal stability of hybrids increases as the ionic strength of the reaction mixture increases. On the other hand, chemical reagents which disrupt hydrogen bonds, such as formamide, urea, dimethyl sulfoxide and alcohols, can greatly reduce the thermal stability of the hybrids.

To ensure specificity of probe for target, it is desirable to have probes which hybridize only under conditions of high stringency. Under conditions of high stringency only highly complementary nucleic acid hybrids will form; hybrids without a sufficient degree of complementarity will not form. Accordingly, the stringency of the assay conditions determines the amount of complementarity needed between two nucleic acid strands to form a hybrid. Stringency is chosen to maximize the difference in stability between the hybrid formed with the target and other nucleic acid sequences.

Proper specificity may be achieved by minimizing the length of perfect complementarity to non-target organisms, avoiding G and C rich regions of homology to non-target sequences, and by constructing the probe to contain as many destabilizing mismatches to nontarget sequences as possible. Whether a probe sequence is useful to detect only a specific type of organism depends largely on the thermal stability difference between probe:target hybrids versus probe:non-target hybrids. In designing probes, the differences in these T_m values should be as large as possible (preferably 2° C.–5° C. or more).

The length of the target nucleic acid sequence, and accordingly the length of the probe sequence, can also be important. In some cases, there may be several sequences from a particular region, varying in location and length, which yield probes with the desired hybridization characteristics. In other cases, one sequence may be significantly better than another which differs merely by a single base. While it is possible for nucleic acids that are not perfectly complementary to hybridize, the longest stretch of perfectly homologous base sequence will generally determine hybrid stability. Oligonucleotide probes of different lengths and base composition may be used. Preferably, oligonucleotide probes are between 10 to 100 and, more preferably, between 15 to 50 bases in length.

Regions of rRNA known to form strong internal structures inhibitory to hybridization are less preferred target regions. Likewise, probes with extensive self-complementarity should be avoided. As explained above, hybridization is the association of two single strands of complementary nucleic acid to form a hydrogen-bonded double strand. It is implicit that if one of the two strands is wholly or partially involved in an intramolecular or intermolecular hybrid it will be less able to participate in the formation of a new intermolecular probe:target hybrid. In the case of rRNA, the molecule is known to form very stable intramolecular hybrids. By designing a probe so that a substantial portion of the targeted sequence is single-stranded, the rate and extent of hybridization between probe and target may be greatly increased.

An rDNA target occurs naturally in a double-stranded form as does the product of the polymerase chain reaction (PCR). These double-stranded targets are naturally inhibitory to hybridization with a probe and require denaturation prior to hybridization. Appropriate denaturation and hybridization conditions are known in the art (e.g., E. M. Southern, *J. Mol. Biol.* 98: 503 (1975)).

Probe Synthesis

Once a presumptive unique target sequence has been identified, a complementary oligonucleotide probe is selected and synthesized. Defined oligonucleotide probes may be produced by any of several well-known methods, including automated solid-phase chemical synthesis using cyanoethylphosphoramidite precursors (Barone et al., *Nucleic Acids Research* 12: 4051 (1984)), and as described in J. Sambrook, E. F. Fritsch and T. Maniatis, *Molecular Cloning*, ch. 11 (2d ed. 1989). Following synthesis and purification of a particular oligonucleotide probe, several different procedures may be utilized to determine the acceptability of the probe in terms of size and purity. One such procedure is polyacrylamide gel electrophoresis. Another such procedure is High Pressure Liquid Chromatography ("HPLC"). These procedures are well known to those skilled in the art.

Once synthesized, selected oligonucleotide probes may be labeled with a reporter group by any of several well-known methods (e.g., supra, J. Sambrook et al.). Useful labels include radioisotopes and non-radioactive reporting groups. Isotopic labels include ^{3}H, ^{35}S, ^{32}P, ^{125}I, ^{57}Co and ^{14}C. Isotopic labels can be introduced into the oligonucleotide by techniques known in the art such as nick translation, end labeling, second strand synthesis, the use of reverse transcription, and by chemical methods. When using radiolabeled probes, hybridization can be detected by autoradiography, scintillation counting, or gamma counting. The detection method selected will depend upon the particular radioisotope used for labeling.

Non-isotopic materials can also be used for labeling and may be introduced internally into the nucleic acid sequence or at the end of the nucleic acid sequence. Modified nucleotides may be incorporated enzymatically or chemically. Chemical modifications of the probe may be performed during or after synthesis of the probe, for example, through the use of non-nucleotide linker groups as described by Arnold et al., entitled "Non-Nucleotide Linking Reagents for Nucleotide Probes," EPO application number 88308766.0, publication number 313219, hereby incorporated by reference herein. Non-isotopic labels include fluorescent molecules, chemiluminescent molecules, enzymes, cofactors, enzyme substrates, haptens or other ligands.

Preferably, the probes are labeled with an acridinium ester. Acridinium ester labeling may be performed as described by Arnold et al., U.S. Pat. No. 5,185,439 entitled "Acridinium Ester Labeling and Purification of Nucleotide Probes" issued Feb. 9, 1993 and hereby incorporated by reference herein.

Helper Probes

The rate of nucleic acid hybridization of an assay probe with its target nucleic acid is enhanced by the use of "Helper Probes" as disclosed in Hogan and Milliman, U.S. Pat. No. 5,030,557 and hereby incorporated by reference herein. Helper probes are selected to hybridize to nucleic acid sequences located near the region targeted by the assay probe. Hybridization of the helper probe alters the secondary and tertiary structure and thereby renders the targeted area of the nucleic acid more accessible for the detection probe. Helper probes to be used with the assay probes described herein include oligonucleotides having the following nucleotide sequences (written 5' to 3'):

(SEQ ID NO: 1) TCATTGACTT GGTGAGCCAT TACCTCAC

(SEQ ID NO: 3) GCCGTGTCTC AGTCCCATTG TGGCTGTTCT

(SEQ ID NO: 4) ATATAAAAGA ACTTTACAAT CTATAAGACC TTCATCGTTC ACGCGGC

(SEQ ID NO: 6) GGCACATAGT TAGCCGATAC TTATTCAAAT GGTACAGTCA AA

(SEQ ID NO: 7) CCTGCGCTCG TTTTACGCCC AGTAAATCCG GATAACGC

(SEQ ID NO: 8) CGTTAAGCAT CTAGATTTAA TACCAAACTT ACAAACCCG

(SEQ ID NO: 9) CCTACTACAC TCTAGGTTTA CAGTTTTTGA TACAGCTAGA

(SEQ ID NO: 10) GCCTTCGCCA CCGGTGTTCT TCCATATATC TA

(SEQ ID NO: 12) CTAATCCTAT TTGCTCCCCA CACTTTCGAG CCTAAGC

(SEQ ID NO: 13) TTTACGGTGT GGACTACTAG GGTAT

(SEQ ID NO: 15) GCGTTAGCTA CAACACCGAC T

(SEQ ID NO: 16) GTAAGGTTCT ACGTGTATTG TCAAATTAAG CAACATGCTC CACCAC

(SEQ ID NO: 18) CGACAACCAT GCACCACCTG TCATATTGTT AACCTCAAC

(SEQ ID NO: 19) TAGCACGTTT GCAGCCCTAG ATATAAGGGG CATGATG

(SEQ ID NO: 21) CGAATTGCAG CCCTCTATCC GAACTGAGAC TAACTTTTTC TG

(SEQ ID NO: 24) GGAACAGGTA TTTCCACTCT GATATGATCA CTAC,

(SEQ ID NO: 25) GCGTAGCGAT GACCTATTTT ACTTGC

(SEQ ID NO: 26) GGATGGGAAC AGGTATTTCC ACTCTGATAT GATCAC,

(SEQ ID NO: 27) GCGTAGCGAT GACCTATTTT ACTTGCGCTA TTTT

(SEQ ID NO: 28) GAGATCAACG GATTAAAGCC TCTTATCAGC TACCCGTTGC TTATCGCAGA TTAGCACG

(SEQ ID NO: 30) CACTTCACCA GGTATCGCTC TGTTAAACTA TGAATTCATT TATA

(SEQ ID NO: 123) CGACATTTAA TGATGATCGT TTACGGTGTG GAC,

(SEQ ID NO: 124) GCCGACATTT AATGATGATC GTTTACGGTG TGGAC,

(SEQ ID NO: 125) CCCAGGCACA TCATTTAATG CGTTAGCTA, RNA equivalents thereto, SEQ ID NOs. 37, 40, 64, 67, 70, 73, 76, 79, 82, 85, 88, 91, 94, 97, 100, 103, 106, 109, 112, 115, 118, 128, 129, 130; oligonucleotides complementary thereto, SEQ ID NOs. 38, 41, 65, 68, 71, 74, 77, 80, 83, 86, 89, 92, 95, 98, 101, 104, 107, 110, 113, 116, 119, 133, 134, 135; and RNA equivalents to the oligonucleotides complementary thereto, SEQ ID Nos. 39, 42, 66, 69, 72, 75, 78, 81, 84, 87, 90, 93, 96, 98, 102, 105, 108, 111, 114, 117, 120, 138, 139, 140.

Preferably, the following hybridization assay probe and helper probe combinations are used:

	Hybridization probe	Helper probes
SEQ ID NOs:	2	1 and 3
SEQ ID NOs:	5	4 and 6
SEQ ID NOs:	8	7 and 9
SEQ ID NOs:	9	8 and 10
SEQ ID NOs:	11	10 and 12
SEQ ID NOs:	14	13 and 15
SEQ ID NOs:	17	16 and 18
SEQ ID NOs:	20	19 and 21
SEQ ID NOs:	22	24 and 25
SEQ ID NOs:	23	26 and 27

-continued

	Hybridization probe	Helper probes
SEQ ID NOs:	29	28 and 30
SEQ ID NOs:	121	123 and 125
SEQ ID NOs:	122	124 and 125

EXAMPLES

Examples are provided below to illustrate different aspects and embodiments of the present invention. These examples are not intended in any way to limit the disclosed invention.

Probes specific for Ureaplasma were identified by sequencing with primers complementary to the 16S and 23S rRNAs of *U. urealyticum* T-960 (CX-8), or from published 5S sequences. The nucleic acid sequence from phylogenetically near neighbors, including *M. genitalium, M. pneumoniae, M. iowae, M. muris, M. pirum* and *M. gallisepticum,* were used as comparisons with the nucleic sequence from *U. urealyticum* to determine variable regions.

The following hybridization assay probe sequences are featured in the examples described below::

(SEQ ID NO: 2) ACCTCTCAGT ACAGCTACGC G
(SEQ ID NO: 5) CATTTCCTAT CTTAGCGTTT CTTCCC
(SEQ ID NO: 8) CGTTAAGCAT CTAGATTTAA TACCAAACTT ACAAACCCG
(SEQ ID NO: 9) CCTACTACAC TCTAGGTTTA CAGTTTTTGA TACAGCTAGA
(SEQ ID NO: 11) GTCAGTGATA GTCCAAGTTG GC
(SEQ ID NO: 14) CGTTCGAGCC GACATTTAAT GATGATCG
(SEQ ID NO: 17) GCGTCGCAAT AGATGTCAAA CCTAG
(SEQ ID NO: 20) CGATTTTGCA GCAGTTTGTA TTAGCCATTG
(SEQ ID NO: 22) GCTATTTTCG GCTCTAGAGT GCTTGACTTC TGTGTTCGGG ATG
(SEQ ID NO: 23) CGGCTCTAGA GTGCTTGACT TCTGTGTTCG
(SEQ ID NO: 29) CAGTAATCTA ATTCTCATTA GACTGAGTTT CCTCATTCG
(SEQ ID NO: 59) CGAACACAGA AGTCAAGCAC TCTAGAGCCG,
(SEQ ID NO: 110) GTGATCATAT CAGAGTGGAA ATACCTGTTC CCATCC,
(SEQ ID NO: 121) CAACACCGAC TCGTTCGAGC, and
(SEQ ID NO: 122) CAACACCGAC CCATTCGG.

The probes were synthesized with a non-nucleotide linker as described by Arnold et al. supra, "Non-Nucleotide Linking Reagents For Nucleotide Probes," then labeled with a chemiluminescent acridinium ester as described by Arnold et al., supra, U.S. Pat. No. 5,185,439. The reactivity and specificity of the probes for *U. urealyticum* were demonstrated using a hybridization and separation format (Example 1, Tables 1–4) or a homogeneous assay format (Examples 2 and 3, Tables 5 and 6; Example 4, Tables 7 and 8). These procedures are described by Arnold et al., supra, "Homogeneous Protection Assay"; Arnold et al., "Polycationic Supports and Nucleic Acid Purification, Separation and Hybridization" EPO application number 88301839.2, publication number 0 281 390 (hereby incorporated by reference herein); and Arnold et al., *Clin. Chem.,* 35:1588 (1989) (hereby incorporated by reference herein).

Results are given in relative light units (RLU). Probes were hybridized to a cell lysate or RNA purified according to J. Sambrook, E. F. Fritsch and T. Maniatis, *Molecular Cloning* (2d ed. 1989). Alternatively, lysates, especially of Mycobacteria, Gram positive organisms, or yeasts, could be obtained utilizing a method described by Murphy et al., "Method for Releasing RNA and DNA from Cells," EPO application number 87303641.2, publication number 288618, hereby incorporated by reference herein. The following examples describe hybridization assay probes targeted to *U. urealyticum* rRNA sequences, or the corresponding gene, and their use in a hybridization assay.

Example 1

This example illustrates the ability of a mixture containing acridinium ester-labeled probes targeted to Ureaplasma 16S rRNA to detect various Ureaplasma strains but not other microorganisms. The mixture contained assay probes having SEQ ID NOs. 2, 5, 8, 9, 11, 14, 17 and 20, and the corresponding unlabeled "Helper Probes" (as described above).

Table 1 presents data using these probes with an excess of RNA released from liquid broth cultures containing 10^6–10^8 organisms. An equal volume of cell lysate and hybridization solution containing 0.19 M lithium succinate pH 5, 0.62 M lithium lauryl sulfate, 3 mM ethylenediaminetetraacetic acid (EDTA), 3 mM ethylene glycol bis (beta-amino ethyl ether) N, N, N', N' tetraacetic acid (EGTA) were mixed and incubated at 60° C. for one hour. Hybrids were then bound to magnetic amine microspheres (Advanced Magnetics, Inc., Cambridge, Mass.) in a solution containing 0.76 M sodium borate pH 7.5, 6% Triton and washed once in a solution containing 80 mM sodium borate pH 10.4. The chemiluminescence associated with the particles, from the hybridized acridinium ester-labeled probes, was measured in a luminometer equipped with automatic injection of 0.1% hydrogen peroxide in 1 mM nitric acid, followed by injection of a 1N sodium hydroxide solution. RLU from a hybridization reaction containing 1 ng of non-target RNA was subtracted from the values shown. The data in Table 1 show that the probes hybridize to known strains or serotypes of *U. urealyticum* found in humans as well as to *U. cati, U. diversum* and *U. gallorale* of animal origin.

Table 2 shows that the probes distinguish Ureaplasma from several closely related Mycoplasma, Acholeplasma, or Spiroplasma species. A net RLU value greater than 300 RLU was considered a positive reaction. An all-bacteria/yeast probe mixture was used as a control to demonstrate the presence of bacterial nucleic acid (data not shown). Hogan et al., supra, entitled "Nucleic Acid Probes for Detection and/or Quantitation of Non-Viral Organisms," gives examples of suitable all-bacteria/yeast probe mixtures. The all-bacteria probe used in the examples described herein is a derivative of all-bacteria probe No. 7 described by Hogan et al., (the all-bacteria probe used in the examples described herein is shifted so that it is four nucleotides shorter on the 5' end but 5 bases longer on the 3' end probe than the Hogan probe No. 7). The yeast probe is a derivative of fungal probe No. 1 described in Hogan et al.

Table 3 shows that the assay probe mixture distinguishes Ureaplasma from members of a panel of urogenital microbes. The all-bacteria/yeast probe mixture was also used as a control in this experiment.

Table 4 shows that the assay probes distinguish Ureaplasma from twenty-seven bacterial genera representing a phylogenetic cross section of microorganisms. Again, the all-bacteria/yeast probe mixture was used as a control in this experiment.

TABLE 1

HYBRIDIZATION OF UREAPLASMA 16S rRNA PROBES WITH UREAPLASMA STRAINS AND SEROTYPES

ATCC NO.	ORGANISM/ STRAIN	SEROTYPE	NET RLU[a]
	U. urealyticum strain		
27813	7	1	634,146
27618	T-960(CX8)	8	592,533
27814	23	2	775,013
27816	58	4	758,427
27619	K510(CX4)	—	906,488
27815	27	3	703,288
27817	354	5	474,113
27818	Pi	6	769,951
27819	Co	7	780,741
29557	K71-21	4	876,253
29558	K42-35	4	933,227
29559	K12-19	4/8	892,978
33175	Vancouver	9	576,453
33695	K2	11	875,684
33696	U24	12	863,070
33697	U26	14	677,350
33698	U38	13	749,523
33699	Western	10	862,237
49228	*U. cati*	—	467,562
43321	*U. diversum*	—	772,938
43346	*U. gallorale*	—	1,161,922

[a]Chemiluminescence was measured in a Gen-Probe LEADER I luminometer and data are expressed in net Relative Light Units (signal minus the negative control containing 1 ng non-Ureaplasma rRNA).

TABLE 2

HYBRIDIZATION OF UREAPLASMA 16S rRNA PROBES WITH OTHER MOLLICUTES

ORGANISM	ATCC NO.	EXPERIMENT NO.	PROBE MIX NET RLU
Mycoplasma fermentans[a]	15474	1	15
Mycoplasma gallisepticum[a]	19610	1	30
Mycoplasma genitalium[a]	33530	1	31
Mycoplasma hominis[a]	23114	1	38
Mycoplasma iowae[a]	33552	1	81
Mycoplasma muris[a]	33757	1	17
Mycoplasma pirum[a]	25960	1	26
Mycoplasma pneumoniae[a]	15531	1	62
Spiroplasma mirum[a]	29335	1	105
Spiroplasma sp. MQ-1[a]	33825	1	66
Acholeplasma laidlawii[c]	29804	2	180
Mycoplasma arthritidis[c]	35943	2	14
Mycoplasma buccale[c]	23636	2	58
Mycoplasma orale[c]	23714	2	−18
Mycoplasma primatum[c]	15497	2	−29
Mycoplasma salivarium[c]	14277	2	11
Ureaplasma urealyticum[b]	27618	2	938

[a]0.10 ng purified RNA.
[b]0.01 ng purified RNA.
[c]Whole cell lysates from 10^7–10^8 organisms.

TABLE 3

HYBRIDIZATION OF UREAPLASMA 16S rRNA PROBES WITH UROGENITAL MICROBES

ORGANISM[a]	ATCC NO.	UREAPLASMA 16S PROBES NET RLU	ALL-BACTERIA/ YEAST PROBES NET RLU
Bacteroides fragilis	23745	43	605,178
Bacteroides ureolyticus	43605	37	112,716
Candida albicans	18804	26	13,380
Chlamydia trachomatis	VR-878	−1	76,109
Clostridium perfringens	13124	−8	419,044
Eikenella corrodens	23834	−13	812,060
Gardnerella vaginalis	14018	11	55,694
Haemophilus influenzae	9795	6	1,203,162
Lactobacillus acidophilus	4356	−10	424,616
Listeria monocytogenes	35152	−8	33,993
Mycobacterium smegmatis	14468	1	14,392
Neisseria gonorrhoeae	19424	122	147,963
Peptostreptococcus anaerobius	27337	−8	290,081
Staphylococcus aureus	12598	29	16,256
Staphylococcus epidermidis	12228	66	4,519
Torulopsis glabrata	2001	0	646,442

[a]Whole cell lysates were tested at a concentration of 10^7 cells per reaction.

TABLE 4

HYBRIDIZATION OF UREAPLASMA 16S rRNA PROBES WITH A PHYLOGENETIC PANEL

ORGANISM[a]	ATCC NO.	UREAPLASMA 16S PROBES NET RLU	ALL-BACTERIA/ YEAST PROBES NET RLU
Ureaplasma urealyticum	27618	1,170	ND
Alcaligenes faecalis	8750	−6	751,053
Bacillus subtilis	6051	14	19,523
Campylobacter jejuni	33560	2	1,079,901
Chromobacterium violaceum	29094	10	1,026,462
Citrobacter freundii	6750	2	758,996
Actinomyces pyogenes	19411	12	148,548
Corynebacterium xerosis	373	38	2,091
Deinococcus radiodurans	35073	−4	78,908
Derxia gummosa	15994	20	753,002
Enterobacter aerogenes	13048	8	967,109
Enterobacter cloacae	10699	5	1,078,720
Enterococcus avium	14025	32	10,594
Enterococcus faecalis	19433	42	32,000
Erwinia herbicola	33243	9	821,862
Escherichia coli	10798	66	959,572
Klebsiella pneumoniae	23357	12	1,326,216
Legionella pneumophila	33152	34	869,560
Micrococcus luteus	9341	50	6,256
Plesiomonas shigelloides	14029	17	837,909
Proteus mirabilis	25933	17	927,223
Pseudomonas aeruginosa	10145	5	1,285,353
Pseudomonas fluorescens	13525	10	1,318,299
Rhodospirillum rubrum	11170	25	563,898
Streptococcus agalactiae	13813	21	204,717
Streptococcus bovis	33317	7	402,823
Vibrio parahaemolyticus	17802	7	1,138,932
Yersinia enterocolitica	9610	7	1,136,326

[a]Whole cell lysates were tested at a concentration of 10^7 cells per reaction. The Ureaplasma sample contained 0.01 ng of *Ureaplasma urealyticum* rRNA.
ND = not done.

Example 2

Hybridization of an acridinium ester-labeled probe, targeted to a 23S rRNA *U. urealyticum* region, to *U. urealyti-*

cum and other bacteria was evaluated. Lysate (L) or purified RNA was hybridized to probe SEQ ID NO. 29 and helper probes SEQ ID NOs. 28 and 30 in 0.05 M lithium succinate pH 5, 0.6 M LiCl, 1% (w/v) lithium lauryl sulfate, 10 mM EDTA, 10 mM EGTA at 60° C. for 15 minutes, followed by addition of 300 μl of 0.6 M sodium borate pH 8.5, 1% Triton X-100 at 60° C. for 5–7 minutes. Samples were read in a luminometer as described in Example 1. The Ureaplasma sample contained 1 μg of *U. urealyticum* rRNA.

As shown in Table 5, probes targeted to 23S rRNA *U. urealyticum* readily distinguish *U. urealyticum* from other organisms including Mycoplasma. The data in this table is reported in RLU without subtracting background and Negative control values. Values greater than about 20,000 to 30,000 RLU were considered positive results in this assay.

TABLE 5

HYBRIDIZATION OF UREAPLASMA-SPECIFIC 23S rRNA PROBES TO OTHER MOLLICUTES AND *E. COLI*

ORGANISM	ATCC NO.	23S PROBE RLU
Mycoplasma arthritidis (L)	35943	746
Mycoplasma buccale (L)	23636	565
Mycoplasma fermentans (L)	15474	948
Mycoplasma iowae (L)	33552	4,241
Mycoplasma muris (L)	33757	4,346
Mycoplasma pirum (L)	25960	596
Mycoplasma primatum (L)	15497	709
Mycoplasma salivarium (L)	14277	629
Spiroplasma sp. MQ-1 (L)	33825	737
Acholeplasma laidlawii	29804	1,052
Mycoplasma gallisepticum	19610	432
Mycoplasma genitalium	33530	4,503
Mycoplasma hominis	23114	450
Mycoplasma orale	23714	945
Mycoplasma pneumoniae	15531	4,073
Spiroplasma mirum	29335	431
Escherichia coli	10798	772
Ureaplasma urealyticum	27618	1,307,260

Example 3

Acridinium ester-labeled probe SEQ ID NOs. 22 or 23 targeted to 5S rRNA was hybridized to an excess of RNA released from cells in the form of cell lysate or purified as described above and assayed as described in Example 2. Probe SEQ ID NO. 22 was hybridized in the presence of helper probes SEQ ID NOs. 24 and 25; probe SEQ ID NO. 23 was hybridized in the presence of helper probes SEQ ID NOs. 26 and 27.

As shown in Table 6, the probes targeted to *Ureaplasma urealyticum* 5S rRNA were able to distinguish this organism from other Mollicutes.

TABLE 6

HYBRIDIZATION OF UREAPLASMA 5S rRNA PROBES TO MOLLICUTES

ORGANISM	ATCC NO.	PROBE SEQ ID NO. 22 RLU	PROBE SEQ ID NO. 23 RLU
Mycoplasma arginini	23838	1,332	3,655
Mycoplasma arthritidis[a]	35943	1,382	3,957
Mycoplasma bovigenitalium[a]	19852	1,395	4,864
Mycoplasma bovis[a]	25523	1,280	4,885
Mycoplasma buccale[a]	23636	1,332	5,762
Mycoplasma californicum[a]	33461	1,466	6,218
Mycoplasma capricolum[a]	23205	1,496	5,064
Mycoplasma faucium[a]	25293	1,466	6,218
Mycoplasma fermentans[a]	15474	2,017	10,572
Mycoplasma gallisepticum	19610	1,355	5,657
Mycoplasma genitalium	33530	1,233	4,721
Mycoplasma muris[a]	33757	5,640	12,462
Mycoplasma iowae[a]	33552	2,537	6,498
Mycoplasma pirum[a]	25960	1,674	7,354
Mycoplasma lipophylum[a]	27790	1,559	5,103
Mycoplasma neurolyticum[a]	19988	1,482	5,861
Mycoplasma orale	23714	1,697	4,362
Mycoplasma pneumoniae[a]	15531	2,129	7,514
Mycoplasma primatum[a]	15497	1,530	4,787
Mycoplasma salivarium[a]	23064	1,662	4,676
Spiroplasma mirum[a]	29335	2,815	7,227
Ureaplasma urealyticum[a]	27815	895,233	676,817
Ureaplasma urealyticum[a]	27619	1,679,357	1,449,564

[a]Whole cell lysates were tested at a concentration of 10^7 cells per reaction.

Example 4

This example describes probes which can distinguish biotype 1 from biotype 2. In the course of probe development it was observed that one probe gave signals substantially lower for biotype 1 lysates than biotype 2 lysates. This suggested sequence variability in the probe region. To identify probe sequences targeted to a particular biotype several strains of *Ureaplasma urealyticum* were analyzed. Using the sequence information, biotype specific probes SEQ. ID. NOs. 121 and 122 were synthesized and labeled with acridinium ester. The probes were hybridized to rRNA from 18 strains of *Ureaplasma urealyticum* as described in Example 2 and the data is presented in Table 7. The signal obtained with the all-bacteria/yeast probe mix provides a quantitative indication of the amount of rRNA in each sample. The biotype 1 probe reacted only with biotype 1 strains; the biotype 2 probe reacted only with biotype 2 strains.

A similar experiment was performed to investigate the specificity of the biotype probes against 18 closely related Mycoplasma species and two Spiroplasma species. Results shown in Table 8 are the net RLU (i.e., the RLU from sample tested minus the RLU from a negative control sample). As seen in Table 8, the biotype-specific *Ureaplasma urealyticum* probes reacted only with their respective specific biotype strains and did not cross-react with any of the other closely related organisms.

TABLE 7

HYBRIDIZATION OF BIOTYPE PROBES

U. urealyticum ATCC NO.	Biotype	PROBE, NET RLU: All-Bacteria/ Yeast	PROBE, NET RLU: Biotype 1	PROBE, NET RLU: Biotype 2
27813	1	141,390	10,830	913
27815	1	95,249	60,145	130
27818	1	87,785	30,091	101
33697	1	83,584	77,891	130
27618	2	120,574	120	117,078

TABLE 7-continued

HYBRIDIZATION OF BIOTYPE PROBES

U. urealyticum ATCC NO.	Biotype	PROBE, NET RLU All-Bacteria/ Yeast	Biotype 1	Biotype 2
27814	2	142,847	5	128,002
27816	2	112,627	89	148,618
27619	2	159,929	958	180,885
27817	2	69,874	108	69,151
27819	2	101,053	61	146,858
29557	2	113,125	143	128,480
29558	2	133,822	55	104,791
29559	2	92,546	644	150,724
33175	2	60,896	93	95,811
33695	2	122,517	106	143,790
33696	2	115,043	183	134,746
33698	2	112,323	3	125,216
33699	2	98,076	125	127,981

TABLE 8

SPECIFICITY OF BIOTYPE PROBES

ORGANISM	ATCC NO.	PROBE, NET RLU All-Bacteria/ Yeast	Biotype 1	Biotype 2
M. arginini	23838	33,238	230	-184
M. arthritidis	35943	141,240	82	82
M. bovigenitalium	19852	9,543	17	26
M. bovis	25523	70,824	-111	96
M. buccale	23636	15,210	-143	31
M. californicum	33461	113,936	77	26
M. capricolum	23205	50,103	-97	95
M. faucium	25293	61,263	84	21
M. fermentans	15474	34,324	2	-16
M. gallisepticum	19610	62,053	-119	31
M. genitalium	33530	104,629	215	-5
M. pirum	25960	59,082	106	93
M. neurolyticum	19988	17,383	95	72
M. orale	23715	29,103	22	113
M. pneumoniae	15531	34,329	-161	-94
M. primatum	15497	40,730	-18	23
M. salivarium	23064	66,612	-80	-60
M. hominis	23114	46,680	-58	36
Sp. mirum	29335	53,887	-19	34
Sp. MQ-1	33825	35,178	-51	24
U. urealy. bio. 1	27815	62,491	42,268	163
U. urealy. bio. 2	27619	108,404	125	136,790

Example 5

This example illustrates the use of assay probes for Ureaplasma of the same sense as the target nucleic acid to detect the products of target nucleic acid amplification. *Ureaplasma urealyticum* rRNA was amplified by incubation at about 37° C. in 100 μL of a solution comprising 0.3 μM of a promoter-primer (SEQ. ID. No. 141), 50 mM Tris-HCl, pH 7.6, 25 mM KCl, 17.5 mM $MgCl_2$, 5 mM dithiothreitol, 2 mM spermidine trihydrochloride, 6.5 mM rATP, 2.5 mM rCTP, 6.5 mM rGTP, 2.5 mM rUTP, 0.2 mM DATP, 0.2 mM dCTP, 0.2 mM dGTP, 0.2 mM dTTP, 600 U MuMLV reverse transcriptase and 400 U T7 RNA polymerase (Kacian et al., supra, entitled "Nucleic Acid Sequence Amplification Method, Composition, and Kit"). The reaction was monitored by removing aliquots at various time points between 15 minutes and 4 hours and assaying for the product using two 5S rRNA probes of the same sense as the target rRNA (SEQ. ID. Nos. 59, 110) and helper probes (SEQ. ID. Nos. 104, 107) using conditions described in Example 2.

TABLE 9

Time of Incubation	RLU 1 fmol target	0.1 fmol target
15 min	5,389	307
30 min	10,360	778
60 min	40,622	5,588
120 min	144,851	13,051
180 min	192,618	16,249
240 min	203,393	20,745

The data shown in Table 9 demonstrates the ability of assay probes targeted to nucleic acid sequences of the opposite sense as the rRNA of the organism to detect the product from a target amplification procedure. As the amplification time increased, more target sequence was produced resulting in increased signal from probe detection.

The data shown in the various examples described above confirm that the novel probes herein described and claimed are capable of distinguishing Ureaplasma from its known nearest phylogenetic neighbors. The data also demonstrates that probes have been designed which can be used to distinguish Ureaplasma biotypes from each other and from nearest known phylogenetic neighbors. Furthermore, complementary oligonucleotide probes, i.e., those having the same sense as the target, are utilized to detect the products of target amplification procedures now being utilized to increase the detection sensitivity of assays for organisms.

Other embodiments are within the following claims.

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(iii) NUMBER OF SEQUENCES: 141

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

-continued

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

TCATTGACTT GGTGAGCCAT TACCTCAC 28

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

ACCTCTCAGT ACAGCTACGC G 21

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

GCCGTGTCTC AGTCCCATTG TGGCTGTTCT 30

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 47
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

ATATAAAAGA ACTTTACAAT CTATAAGACC TTCATCGTTC ACGCGGC 47

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

CATTTCCTAT CTTAGCGTTT CTTCCC 26

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 42
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

GGCACATAGT TAGCCGATAC TTATTCAAAT GGTACAGTCA AA 42

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 38
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

-continued

CCTGCGCTCG TTTTACGCCC AGTAAATCCG GATAACGC 38

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

CGTTAAGCAT CTAGATTTAA TACCAAACTT ACAAACCCG 39

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 40
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

CCTACTACAC TCTAGGTTTA CAGTTTTTGA TACAGCTAGA 40

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 32
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

GCCTTCGCCA CCGGTGTTCT TCCATATATC TA 32

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

GTCAGTGATA GTCCAAGTTG GC 22

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 37
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

CTAATCCTAT TTGCTCCCCA CACTTTCGAG CCTAAGC 37

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

-continued

TTTACGGTGT GGACTACTAG GGTAT 25

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

CGTTCGAGCC GACATTTAAT GATGATCG 28

(2) INFORMATION FOR SEQ ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

GCGTTAGCTA CAACACCGAC T 21

(2) INFORMATION FOR SEQ ID NO: 16:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

GTAAGGTTCT ACGTGTATTG TCAAATTAAG CAACATGCTC CACCAC 46

(2) INFORMATION FOR SEQ ID NO: 17:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

GCGTCGCAAT AGATGTCAAA CCTAG 25

(2) INFORMATION FOR SEQ ID NO: 18:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

CGACAACCAT GCACCACCTG TCATATTGTT AACCTCAAC 39

(2) INFORMATION FOR SEQ ID NO: 19:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 37
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

TAGCACGTTT GCAGCCCTAG ATATAAGGGG CATGATG 37

-continued

(2) INFORMATION FOR SEQ ID NO: 20:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

CGATTTTGCA GCAGTTTGTA TTAGCCATTG 30

(2) INFORMATION FOR SEQ ID NO: 21:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 42
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

CGAATTGCAG CCCTCTATCC GAACTGAGAC TAACTTTTTC TG 42

(2) INFORMATION FOR SEQ ID NO: 22:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 43
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

GCTATTTTCG GCTCTAGAGT GCTTGACTTC TGTGTTCGGG ATG 43

(2) INFORMATION FOR SEQ ID NO: 23:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

CGGCTCTAGA GTGCTTGACT TCTGTGTTCG 30

(2) INFORMATION FOR SEQ ID NO: 24:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 34
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

GGAACAGGTA TTTCCACTCT GATATGATCA CTAC 34

(2) INFORMATION FOR SEQ ID NO: 25:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

GCGTAGCGAT GACCTATTTT ACTTGC 26

-continued

(2) INFORMATION FOR SEQ ID NO: 26:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 36
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

GGATGGGAAC AGGTATTTCC ACTCTGATAT GATCAC 36

(2) INFORMATION FOR SEQ ID NO: 27:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 34
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

CGTAGCGAT GACCTATTTT ACTTGCGCTA TTTT 34

(2) INFORMATION FOR SEQ ID NO: 28:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

GAGATCAACG GATTAAAGCC TCTTATCAGC TACCCGTTGC TTATCGCAGA TTAGCACG 58

(2) INFORMATION FOR SEQ ID NO: 29:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

CAGTAATCTA ATTCTCATTA GACTGAGTTT CCTCATTCG 39

(2) INFORMATION FOR SEQ ID NO: 30:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 44
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

CACTTCACCA GGTATCGCTC TGTTAAACTA TGAATTCATT TATA 44

(2) INFORMATION FOR SEQ ID NO: 31:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

ACCUCUCAGU ACAGCUACGC G 21

-continued

(2) INFORMATION FOR SEQ ID NO: 32:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

CGCGTAGCTG TACTGAGAGG T 21

(2) INFORMATION FOR SEQ ID NO: 33:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

CGCGUAGCUG UACUGAGAGG U 21

(2) INFORMATION FOR SEQ ID NO: 34:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

CAUUUCCUAU CUUAGCGUUU CUUCCC 26

(2) INFORMATION FOR SEQ ID NO: 35:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

GGGAAGAAAC GCTAAGATAG GAAATG 26

(2) INFORMATION FOR SEQ ID NO: 36:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

GGGAAGAAAC GCUAAGAUAG GAAAUG 26

(2) INFORMATION FOR SEQ ID NO: 37:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

CGUUAAGCAU CUAGAUUUAA UACCAAACUU ACAAACCCG 39

(2) INFORMATION FOR SEQ ID NO: 38:

-continued

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

CGGGTTTGTA AGTTTGGTAT TAAATCTAGA TGCTTAACG 39

(2) INFORMATION FOR SEQ ID NO: 39:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

CGGGUUUGUA AGUUUGGUAU UAAAUCUAGA UGCUUAACG 39

(2) INFORMATION FOR SEQ ID NO: 40:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 40
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

CCUACUACAC UCUAGGUUUA CAGUUUUUGA UACAGCUAGA 40

(2) INFORMATION FOR SEQ ID NO: 41:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 40
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

TCTAGCTGTA TCAAAAACTG TAAACCTAGA GTGTAGTAGG 40

(2) INFORMATION FOR SEQ ID NO: 42:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 40
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

UCUAGCUGUA UCAAAAACUG UAAACCUAGA GUGUAGUAGG 40

(2) INFORMATION FOR SEQ ID NO: 43:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

GUCAGUGAUA GUCCAAGUUG GC 22

(2) INFORMATION FOR SEQ ID NO: 44:

-continued

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

GCCAACTTGG ACTATCACTG AC 22

(2) INFORMATION FOR SEQ ID NO: 45:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

GCCAACUUGG ACUAUCACUG AC 22

(2) INFORMATION FOR SEQ ID NO: 46:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

CGUUCGAGCC GACAUUUAAU GAUGAUCG 28

(2) INFORMATION FOR SEQ ID NO: 47:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

CGATCATCAT TAAATGTCGG CTCGAACG 28

(2) INFORMATION FOR SEQ ID NO: 48:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

CGAUCAUCAU UAAAUGUCGG CUCGAACG 28

(2) INFORMATION FOR SEQ ID NO: 49:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 49:

GCGUCGCAAU AGAUGUCAAA CCUAG 25

(2) INFORMATION FOR SEQ ID NO: 50:

(i) SEQUENCE CHARACTERISTICS:

-continued

(A) LENGTH: 25
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 50:

CTAGGTTTGA CATCTATTGC GACGC 25

(2) INFORMATION FOR SEQ ID NO: 51:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

CUAGGUUUGA CAUCUAUUGC GACGC 25

(2) INFORMATION FOR SEQ ID NO: 52:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 52:

CGAUUUUGCA GCAGUUUGUA UUAGCCAUUG 30

(2) INFORMATION FOR SEQ ID NO: 53:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

CAATGGCTAA TACAAACTGC TGCAAAATCG 30

(2) INFORMATION FOR SEQ ID NO: 54:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 54:

CAAUGGCUAA UACAAACUGC UGCAAAAUCG 30

(2) INFORMATION FOR SEQ ID NO: 55:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 43
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 55:

GCUAUUUUCG GCUCUAGAGU GCUUGACUUC UGUGUUCGGG AUG 43

(2) INFORMATION FOR SEQ ID NO: 56:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 43

-continued

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 56:

CATCCCGAAC ACAGAAGTCA AGCACTCTAG AGCCGAAAAT AGC 43

(2) INFORMATION FOR SEQ ID NO: 57:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 43
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 57:

CAUCCCGAAC ACAGAAGUCA AGCACUCUAG AGCCGAAAAU AGC 43

(2) INFORMATION FOR SEQ ID NO: 58:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 58:

CGGCUCUAGA GUGCUUGACU UCUGUGUUCG 30

(2) INFORMATION FOR SEQ ID NO: 59:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 59:

CGAACACAGA AGTCAAGCAC TCTAGAGCCG 30

(2) INFORMATION FOR SEQ ID NO: 60:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 60:

CGAACACAGA AGUCAAGCAC UCUAGAGCCG 30

(2) INFORMATION FOR SEQ ID NO: 61:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 61:

CAGUAAUCUA AUUCUCAUUA GACUGAGUUU CCUCAUUCG 39

(2) INFORMATION FOR SEQ ID NO: 62:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39
(B) TYPE: nucleic acid

-continued

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 62:

CGAATGAGGA AACTCAGTCT AATGAGAATT AGATTACTG 39

(2) INFORMATION FOR SEQ ID NO: 63:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 63:

CGAAUGAGGA AACUCAGUCU AAUGAGAAUU AGAUUACUG 39

(2) INFORMATION FOR SEQ ID NO: 64:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 64:

UCAUUGACUU GGUGAGCCAU UACCUCAC 28

(2) INFORMATION FOR SEQ ID NO: 65:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 65:

GTGAGGTAAT GGCTCACCAA GTCAATGA 28

(2) INFORMATION FOR SEQ ID NO: 66:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 66:

GUGAGGUAAU GGCUCACCAA GUCAAUGA 28

(2) INFORMATION FOR SEQ ID NO: 67:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 67:

GCCGUGUCUC AGUCCCAUUG UGGCUGUUCU 30

(2) INFORMATION FOR SEQ ID NO: 68:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

-continued

(D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 68:

AGAACAGCCA CAATGGGACT GAGACACGGC 30

(2) INFORMATION FOR SEQ ID NO: 69:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 69:

AGAACAGCCA CAAUGGGACU GAGACACGGC 30

(2) INFORMATION FOR SEQ ID NO: 70:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 47
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 70:

AUAUAAAAGA ACUUUACAAU CUAUAAGACC UUCAUCGUUC ACGCGGC 47

(2) INFORMATION FOR SEQ ID NO: 71:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 47
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 71:

GCCGCGTGAA CGATGAAGGT CTTATAGATT GTAAAGTTCT TTTATAT 47

(2) INFORMATION FOR SEQ ID NO: 72:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 47
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 72:

GCCGCGUGAA CGAUGAAGGU CUUAUAGAUU GUAAAGUUCU UUUAUAU 47

(2) INFORMATION FOR SEQ ID NO: 73:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 42
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 73:

GGCACAUAGU UAGCCGAUAC UUAUUCAAAU GGUACAGUCA AA 42

(2) INFORMATION FOR SEQ ID NO: 74:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 42
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

-continued

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 74:

TTTGACTGTA CCATTTGAAT AAGTATCGGC TAACTATGTG CC 42

(2) INFORMATION FOR SEQ ID NO: 75:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 42
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 75:

UUUGACUGUA CCAUUUGAAU AAGUAUCGGC UAACUAUGUG CC 42

(2) INFORMATION FOR SEQ ID NO: 76:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 38
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 76:

CCUGCGCUCG UUUUACGCCC AGUAAAUCCG GAUAACGC 38

(2) INFORMATION FOR SEQ ID NO: 77:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 38
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 77:

GCGTTATCCG GATTTACTGG GCGTAAAACG AGCGCAGG 38

(2) INFORMATION FOR SEQ ID NO: 78:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 38
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 78:

GCGUUAUCCG GAUUUACUGG GCGUAAAACG AGCGCAGG 38

(2) INFORMATION FOR SEQ ID NO: 79:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 32
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 79:

GCCUUCGCCA CCGGUGUUCU UCCAUAUAUC UA 32

(2) INFORMATION FOR SEQ ID NO: 80:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 32
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

-continued

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 80:

TAGATATATG GAAGAACACC GGTGGCGAAG GC 32

(2) INFORMATION FOR SEQ ID NO: 81:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 32
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 81:

UAGAUAUAUG GAAGAACACC GGUGGCGAAG GC 32

(2) INFORMATION FOR SEQ ID NO: 82:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 37
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 82:

CUAAUCCUAU UUGCUCCCCA CACUUUCGAG CCUAAGC 37

(2) INFORMATION FOR SEQ ID NO: 83:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 37
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 83:

GCTTAGGCTC GAAAGTGTGG GGAGCAAATA GGATTAG 37

(2) INFORMATION FOR SEQ ID NO: 84:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 37
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 84:

GCUUAGGCUC GAAAGUGUGG GGAGCAAAUA GGAUUAG 37

(2) INFORMATION FOR SEQ ID NO: 85:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 85:

UUUACGGUGU GGACUACUAG GGUAU 25

(2) INFORMATION FOR SEQ ID NO: 86:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 86:

-continued

ATACCCTAGT AGTCCACACC GTAAA 25

(2) INFORMATION FOR SEQ ID NO: 87:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 87:

AUACCCUAGU AGUCCACACC GUAAA 25

(2) INFORMATION FOR SEQ ID NO: 88:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 88:

GCGUUAGCUA CAACACCGAC U 21

(2) INFORMATION FOR SEQ ID NO: 89:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 89:

AGTCGGTGTT GTAGCTAACG C 21

(2) INFORMATION FOR SEQ ID NO: 90:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 90:

AGUCGGUGUU GUAGCUAACG C 21

(2) INFORMATION FOR SEQ ID NO: 91:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 91:

GUAAGGUUCU ACGUGUAUUG UCAAAUUAAG CAACAUGCUC CACCAC 46

(2) INFORMATION FOR SEQ ID NO: 92:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 92:

-continued

GTGGTGGAGC ATGTTGCTTA ATTTGACAAT ACACGTAGAA CCTTAC 46

(2) INFORMATION FOR SEQ ID NO: 93:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 93:

GUGGUGGAGC AUGUUGCUUA AUUUGACAAU ACACGUAGAA CCUUAC 46

(2) INFORMATION FOR SEQ ID NO: 94:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 94:

CGACAACCAU GCACCACCUG UCAUAUUGUU AACCUCAAC 39

(2) INFORMATION FOR SEQ ID NO: 95:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 95:

GTTGAGGTTA ACAATATGAC AGGTGGTGCA TGGTTGTCG 39

(2) INFORMATION FOR SEQ ID NO: 96:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 96:

GUUGAGGUUA ACAAUAUGAC AGGUGGUGCA UGGUUGUCG 39

(2) INFORMATION FOR SEQ ID NO: 97:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 37
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 97:

UAGCACGUUU GCAGCCCUAG AUAUAAGGGG CAUGAUG 37

(2) INFORMATION FOR SEQ ID NO: 98:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 37
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 98:

CATCATGCCC CTTATATCTA GGGCTGCAAA CGTGCTA 37

-continued

(2) INFORMATION FOR SEQ ID NO: 99:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 37
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 99:

CAUCAUGCCC CUUAUAUCUA GGGCUGCAAA CGUGCUA 37

(2) INFORMATION FOR SEQ ID NO: 100:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 42
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 100:

CGAAUUGCAG CCCUCUAUCC GAACUGAGAC UAACUUUUUC UG 42

(2) INFORMATION FOR SEQ ID NO: 101:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 42
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 101:

CAGAAAAAGT TAGTCTCAGT TCGGATAGAG GGCTGCAATT CG 42

(2) INFORMATION FOR SEQ ID NO: 102:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 42
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 102:

CAGAAAAAGU UAGUCUCAGU UCGGAUAGAG GGCUGCAAUU CG 42

(2) INFORMATION FOR SEQ ID NO: 103:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 34
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 103:

GGAACAGGUA UUUCCACUCU GAUAUGAUCA CUAC 34

(2) INFORMATION FOR SEQ ID NO: 104:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 34
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 104:

GTAGTGATCA TATCAGAGTG GAAATACCTG TTCC 34

-continued

(2) INFORMATION FOR SEQ ID NO: 105:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 34
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 105:

GUAGUGAUCA UAUCAGAGUG GAAAUACCUG UUCC 34

(2) INFORMATION FOR SEQ ID NO: 106:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 106:

GCGUAGCGAU GACCUAUUUU ACUUGC 26

(2) INFORMATION FOR SEQ ID NO: 107:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 107:

GCAAGTAAAA TAGGTCATCG CTACGC 26

(2) INFORMATION FOR SEQ ID NO: 108:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 108:

GCAAGUAAAA UAGGUCAUCG CUACGC 26

(2) INFORMATION FOR SEQ ID NO: 109:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 36
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 109:

GGAUGGGAAC AGGUAUUUCC ACUCUGAUAU GAUCAC 36

(2) INFORMATION FOR SEQ ID NO: 110:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 36
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 110:

GTGATCATAT CAGAGTGGAA ATACCTGTTC CCATCC 36

-continued

(2) INFORMATION FOR SEQ ID NO: 111:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 36
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 111:

GUGAUCAUAU CAGAGUGGAA AUACCUGUUC CCAUCC 36

(2) INFORMATION FOR SEQ ID NO: 112:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 34
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 112:

GCGUAGCGAU GACCUAUUUU ACUUGCGCUA UUUU 34

(2) INFORMATION FOR SEQ ID NO: 113:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 34
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 113:

AAAATAGCGC AAGTAAAATA GGTCATCGCT ACGC 34

(2) INFORMATION FOR SEQ ID NO: 114:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 34
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 114:

AAAAUAGCGC AAGUAAAAUA GGUCAUCGCU ACGC 34

(2) INFORMATION FOR SEQ ID NO: 115:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 115:

GAGAUCAACG GAUUAAAGCC UCUUAUCAGC UACCCGUUGC UUAUCGCAGA UUAGCACG 58

(2) INFORMATION FOR SEQ ID NO: 116:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 116:

CGTGCTAATC TGCGATAAGC AACGGGTAGC TGATAAGAGG CTTTAATCCG TTGATCTC 58

(2) INFORMATION FOR SEQ ID NO: 117:

-continued

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 117:

CGUGCUAAUC UGCGAUAAGC AACGGGUAGC UGAUAAGAGG CUUUAAUCCG UUGAUCUC 58

(2) INFORMATION FOR SEQ ID NO: 118:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 44
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 118:

CACUUCACCA GGUAUCGCUC UGUUAAACUA UGAAUUCAUU UAUA 44

(2) INFORMATION FOR SEQ ID NO: 119:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 44
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 119:

TATAAATGAA TTCATAGTTT AACAGAGCGA TACCTGGTGA AGTG 44

(2) INFORMATION FOR SEQ ID NO: 120:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 44
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 120:

UAUAAAUGAA UUCAUAGUUU AACAGAGCGA UACCUGGUGA AGUG 44

(2) INFORMATION FOR SEQ ID NO: 121:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 121:

CAACACCGAC TCGTTCGAGC 20

(2) INFORMATION FOR SEQ ID NO: 122:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 122:

CAACACCGAC CCATTCGG 18

(2) INFORMATION FOR SEQ ID NO: 123:

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(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 123:

CGACATTTAA TGATGATCGT TTACGGTGTG GAC 33

(2) INFORMATION FOR SEQ ID NO: 124:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 35
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 124:

GCCGACATTT AATGATGATC GTTTACGGTG TGGAC 35

(2) INFORMATION FOR SEQ ID NO: 125:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 125:

CCCAGGCACA TCATTTAATG CGTTAGCTA 29

(2) INFORMATION FOR SEQ ID NO: 126:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 126:

CAACACCGAC UCGUUCGAGC 20

(2) INFORMATION FOR SEQ ID NO: 127:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 127:

CAACACCGAC CCAUUCGG 18

(2) INFORMATION FOR SEQ ID NO: 128:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 128:

CGACAUUUAA UGAUGAUCGU UUACGGUGUG GAC 33

(2) INFORMATION FOR SEQ ID NO: 129:

(i) SEQUENCE CHARACTERISTICS:

-continued

(A) LENGTH: 35
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 129:

GCCGACAUUU AAUGAUGAUC GUUUACGGUG UGGAC 35

(2) INFORMATION FOR SEQ ID NO: 130:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 130:

CCCAGGCACA UCAUUUAAUG CGUUAGCUA 29

(2) INFORMATION FOR SEQ ID NO: 131:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 131:

GCTCGAACGA GTCGGTGTTG 20

(2) INFORMATION FOR SEQ ID NO: 132:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 132:

CCGAATGGGT CGGTGTTG 18

(2) INFORMATION FOR SEQ ID NO: 133:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 133:

GTCCACACCG TAAACGATCA TCATTAAATG TCG 33

(2) INFORMATION FOR SEQ ID NO: 134:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 35
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 134:

GTCCACACCG TAAACGATCA TCATTAAATG TCGGC 35

(2) INFORMATION FOR SEQ ID NO: 135:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29

-continued

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 135:

TAGCTAACGC ATTAAATGAT GTGCCTGGG 29

(2) INFORMATION FOR SEQ ID NO: 136:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 136:

GCUCGAACGA GUCGGUGUUG 20

(2) INFORMATION FOR SEQ ID NO: 137:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 137:

CCGAAUGGGU CGGUGUUG 18

(2) INFORMATION FOR SEQ ID NO: 138:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 138:

GUCCACACCG UAAACGAUCA UCAUUAAAUG UCG 33

(2) INFORMATION FOR SEQ ID NO: 139:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 35
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 139:

GUCCACACCG UAAACGAUCA UCAUUAAAUG UCGGC 35

(2) INFORMATION FOR SEQ ID NO: 140:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 140:

UAGCUAACGC AUUAAAUGAU GUGCCUGGG 29

(2) INFORMATION FOR SEQ ID NO: 141:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53
(B) TYPE: nucleic acid

-continued

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 141:

AATTTAATAC GACTCACTAT AGGGAGAGCG TAGCGATGAC CTATTTTACT TGC 53

What is claimed is:

1. A hybridization assay probe 10 to 100 nucleotides in length comprising an oligonucleotide sufficiently complementary to a *Ureaplasma urealyticum* target nucleic acid sequence to form a detectable probe:target hybrid with said *Ureaplasma urealyticum* target nucleic acid sequence under stringent hybridization assay conditions, wherein said *Ureaplasma urealyticum* target nucleic acid sequence is selected from the group consisting of

SEQ ID NO: 31: ACCUCUCAGU ACAGCUACGC G,
SEQ ID NO: 33: CGCGUAGCUG UACUGAGAGG U,
SEQ ID NO: 37: CGUUAAGCAU CUAGAUUUAA UACCAAACUU ACAAACCCG,
SEQ ID NO: 39: CGGGUUUGUA AGUUUGGUAU UAAAUCUAGA UGCUUAACG,
SEQ ID NO: 40: CCUACUACAC UCUAGGUUUA CAGUUUUUGA UACAGCUAGA,
SEQ ID NO: 42: UCUAGCUGUA UCAAAAACUG UAAACCUAGA GUGUAGUAGG,
SEQ ID NO: 43: GUCAGUGAUA GUCCAAGUUG GC,
SEQ ID NO: 45: GCCAACUUGG ACUAUCACUG AC,
SEQ ID NO: 61: CAGUAAUCUA AUUCUCAUUA GACUGAGUUU CCUCAUUCG,
SEQ ID NO: 63: CGAAUGAGGA AACUCAGUCU AAUGAGAAUU AGAUUACUG,
SEQ ID NO; 109: GGAUGGGAAC AGGUAUUUCC ACUCUGAUAU GAUCAC, and
SEQ ID NO: 111: GUGAUCAUAU CAGAGUGGAA AUACCUGUC CCAUCC;

wherein under said stringent hybridization assay conditions said hybridization assay probe does not form a detectable probe:non-target hybrid with nucleic acid from *Mycoplasma hominis*.

2. The hybridization assay probe of claim 1, wherein said hybridization assay probe also does not form said detectable probe:non-target hybrid with nucleic acid from *Mycoplasma genizalium* and *Mycoplasma pneumoniae*.

3. The hybridization assay probe of claim 1, wherein said hybridizaton assay probe also does not form said detectable probe:non-target hybrid with nucleic acid from *Mycoplasma orale, Mycoplasma fermentans, Mycoplasma capricolum, Mycoplasma lipophilum,* and *Mycoplasma salivarium*.

4. The hybridization assay probe of claim 2, wherein said target *Ureaplasma urealyticum* nucleic acid sequence is selected from the group consisting of SEQ ID NO: 31 and SEQ ID NO: 33.

5. The hybridization assay probe of claim 2, wherein said target *Ureaplasma urealyticum* nucleic acid sequence is selected from the group consisting of SEQ ID NO: 37 and SEQ ID NO: 39.

6. The hybridization assay probe of claim 2, wherein said target *Ureaplasma urealyticum* nucleic acid sequence is selected from the group consisting of SEQ ID NO: 40 and SEQ ID NO: 42.

7. The hybridization assay probe of claim 2, wherein said target *Ureaplasma urealyticum* nucleic acid sequence is selected from the group consisting of SEQ ID NO: 43 and SEQ ID NO: 45.

8. The hybridization assay probe of claim 2, wherein said target *Ureaplasma urealyticum* nucleic acid sequence is selected from the group consisting of SEQ ID NO: 61 and SEQ ID NO: 63.

9. The hybridization assay probe of claim 2, wherein said target *Ureaplasma urealyticum* nucleic acid sequence is selected from the group consisting of SEQ ID NO: 109 and SEQ ID NO: 111.

10. A hybridization assay probe for detecting Ureaplasma under stringent hybridization assay conditions which is 21 to 100 nucleotides in length and comprises a nucleotide base sequence selected from the group consisting of:

SEQ ID NO: 2: ACCTCTCAGT ACAGCTACGC G,
SEQ ID NO: 8: CGTTAAGCAT CTAGATTTAA TACCAAACTT ACAAACCCG,
SEQ ID NO: 9: CCTACTACAC TCTAGGTTTA CAGTTTTTGA TACAGCTAGA,
SEQ ID NO: 11: CTCAGTGATA GTCCAAGTTG GC,
SEQ ID NO: 20: CGATTTTGCA GCAGTTTGTA TTAGCCATTG,
SEQ ID NO: 26: GGATGGGAAC AGGTATTTCC ACTCTGATAT GATCAC,
SEQ ID NO: 29: CAGTAATCTA ATTCTCATTA GACTGAGTTT CCTCATTCG,
SEQ ID NO: 31: ACCUCUCAGU ACAGCUACGC G,
SEQ ID NO: 32: CGCGTAGCTG TACTGAGAGG T,
SEQ ID NO: 33: CGCGUAGCUG UACUGAGAGG U,
SEQ ID NO: 37: CGUUAAGCAU CUAGAUUUAA UACCAAACUU ACAAACCCG,
SEQ ID NO: 38: CGGGTTTGTA AGTTTGGTAT TAAATCTAGA TGCTTAACG,
SEQ ID NO: 39: CGGGUUUGUA AGUUUGGUAU UAAAUCUAGA UGCUUAACG,
SEQ ID NO: 40: CCUACUACAC UCUAGGUUUA CAGUUUUUGA UACAGCUAGA,
SEQ ID NO: 41: TCTAGCTGTA TCAAAAACTG TAAACCTAGA GTGTAGTAGG,
SEQ ID NO: 42: UCUAGCUGUA UCAAAAACUG UAAACCUAGA GUGUAGUAGG,
SEQ ID NO: 43: GUCAGUGAUA GUCCAAGUUG GC,
SEQ ID NO: 44: GCCAACTTGG ACTATCACTG AC,
SEQ ID NO: 45: GCCAACUUGG ACUAUCACUG AC,
SEQ ID NO: 52: CGAUUUUGCA GCAGUUUGUA UUAGCCAUUG,
SEQ ID NO: 53: CAATGGCTAA TACAAACTGC TGCAAAATCG,
SEQ ID NO: 61: CAGUAAUCUA AUUCUCAUUA GACUGAGUUU CCUCAUUCG,
SEQ ID NO: 62: CGAATGAGGA AACTCAGTCT AATGAGAATT AGATTACTG,
SEQ ID NO: 63: CGAAUGAGGA AACUCAGUCU AAUGAGAAUU AGAUUACUG,

SEQ ID NO: 109: GGAUGGGAAC AGGUAUUUCC ACUCUGAUAU GAUCAC,

SEQ ID NO: 110: GTGATCATAT CAGAGTGGAA ATACCTGTTC CCATCC, and

SEQ ID NO: 111 GUGAUCAUAU CAGAGUGGAA AUACCUGUUC CCAUCC;

wherein said hybridization assay probe hybridizes to *Ureaplasma urealyticum* nucleic acid to form a detectable probe:target hybrid under stringent hybridization assay conditions, but does not hybridize to nucleic acid from *Mycoplasma genitalium, Mycoplasma hominis* and *Mycoplasma pneumoniae* to form a detectable probe:non-target hybrid under said stringent hybridization assay conditions.

11. The hybridization assay probe of claim **10**, wherein said nucleotide base sequence is selected from the group consisting of SEQ ID NO: 2, SEQ ID NO: 31, SEQ ID NO: 32, and SEQ ID NO: 33.

12. The hybridization assay probe of claim **10**, wherein said nucleotide base sequence is selected from the group consisting of SEQ ID NO: 8, SEQ ID NO: 37, SEQ ID NO: 38, and SEQ ID NO: 39.

13. The hybridization assay probe of claim **10**, wherein said nucleotide base sequence is selected from the group consisting of SEQ ID NO: 9, SEQ ID NO: 40, SEQ ID NO: 41, and SEQ ID NO: 42.

14. The hybridization assay probe of claim **10**, wherein said nucleotide base sequence is selected from the group consisting of SEQ ID NO: 11, SEQ ID NO: 43, SEQ ID NO: 44, and SEQ ID NO: 45.

15. The hybridization assay probe of claim **10**, wherein said nucleotide base sequence is selected from the group consisting of SEQ ID NO: 20, SEQ ID NO: 52, and SEQ ID NO: 53.

16. The hybridization assay probe of claim **10**, wherein said nucleotide base sequence is selected from the group consisting of SEQ ID NO: 26, SEQ ID NO: 109, SEQ ID NO: 110, and SEQ ID NO: 111.

17. The hybridization assay probe of claim **10**, wherein said nucleotide base sequence is selected from the group consisting of SEQ ID NO: 29, SEQ ID NO: 61, SEQ ID NO: 62, and SEQ ID NO: 63.

18. The hybridization assay probe of any one of claims **11, 12, 13, 14, 15, 16**, and **17**, wherein said hybridization assay probe consists of said nucleotide base sequence and one or more reporter groups.

19. A hybridization assay probe 10 to 100 nucleotides in length comprising an oligonucleotide sufficiently complementary to a *Ureaplasma urealyticum* biotype specific target nucleic acid sequence to form a detectable probe:target hybrid under stringent hybridization assay conditions with either *Ureaplasma urealyticum* biotype 1 nucleic acid or *Ureaplasma urealyticum* biotype 2 nucleic acid, wherein said hybridization assay probe does not form said detectable probe:target hybrid with both *Ureaplasma urealyticum* biotype 1 nucleic acid and *Ureaplasma urealyticum* biotype 2 nucleic acid under said stringent hybridization assay conditions, said biotype specific target nucleic acid sequence being selected from the group consisting of:

SEQ ID NO: 126: CAACACCGAC UCGUUCGAGC,

SEQ ID NO: 127: CAACACCGAC CCAUUCGG,

SEQ ID NO: 136: GCUCGAACGA GUCGGUGUUG, and

SEQ ID NO: 137: CCGAAUGGGU CGGUGUUG; and

wherein said hybridization assay probe does not hybridize to nucleic acid from *Mycoplasma genitalium, Mycoplasma hominis* and *Mycoplasma pneumoniae* to form a detectable probe:non-target hybrid under said stringent hybridization assay conditions.

20. The probe of claim **19**, wherein said biotype specific target nucleic acid sequence is either SEQ ID NO: 126 or SEQ ID NO: 136.

21. The probe of claim **19**, wherein said biotype specific target nucleic acid sequence is either SEQ ID NO: 127 or SEQ ID NO: 137.

22. A hybridization assay probe for distinguishing between different *Ureaplasma urealyticum* biotypes which is 20 to 100 nucleotides in length and comprises a nucleotide base sequence selected from the group consisting of:

SEQ ID NO: 121: CAACACCGAC TCGTTCGAGC,

SEQ ID NO: 126: CAACACCGAC UCGUUCGAGC,

SEQ ID NO: 131: GCTCGAACGA GTCGGTGTTG, and

SEQ ID NO: 136: GCUCGAACGA GUCGGUGUUG;

provided that under stringent hybridization assay conditions said hybridization assay probe hybridizes with *Ureaplasma urealyticum* biotype 2 nucleic acid to form a detectable probe:target hybrid, and said hybridization assay probe does not form said detectable probe:target hybrid with *Ureaplasma urealyticum* biotype 1 nucleic acid under said stringent hybridization assay conditions,

further provided that said hybridization assay probe does not hybridize to nucleic acid from *Mycoplasma genitalium, Mycoplasma hominis* and *Mycoplasma pneumoniae* to form a detectable probe:non-target hybrid under said stringent hybridization assay conditions.

23. The probe of claim **22**, wherein said hybridization assay probe consists of said nucleotide base sequence and one or more reporter groups.

24. A hybridization assay probe for distinguishing between different *Ureaplasma urealyticum* biotypes which is 18 to 100 nucleotides in length and comprises a nucleotide base sequence selected from the group consisting of

SEQ ID NO: 122: CAACACCGAC CCATTCGG,

SEQ ID NO: 127: CAACACCGAC CCAUUCGG,

SEQ ID NO: 132: CCGAATGGGT CGGTGTTG, and

SEQ ID NO: 137: CCGAAUGGGU CGGUGUUG

provided that under stringent hybridization assay conditions said hybridization assay probe hybridizes with *Ureaplasma urealyticum* biotype 1 nucleic acid to form a detectable probe:target hybrid, and said hybridization assay probe does not form said detectable probe:target hybrid with *Ureaplasma urealyticum* biotype 2 nucleic acid under said stringent hybridization assay conditions,

further provided that said hybridization assay probe does not hybridize to nucleic acid from *Mycoplasma genitalium, Mycoplasma hominis* and *Mycoplasma pneumoniae* to form a detectable probe:non-target hybrid under said stringent hybridization assay conditions.

25. The probe of claim **24**, wherein said hybridization assay probe consists of said nucleotide base sequence and one or more reporter groups.

26. A probe mix comprising:

a) a hybridization assay probe for detecting Ureaplasma under stringent hybridization assay conditions which is 21 to 100 nucleotides in length and comprises a nucleotide base sequence selected from the group consisting of:

SEQ ID NO: 2: ACCTCTCAGT ACAGCTACGC G,

SEQ ID NO: 8: CGTTAAGCAT CTAGATTTAA TACCAAACTT ACAAACCCG,

SEQ ID NO: 9: CCTACTACAC TCTAGGTTTA CAGTTTTTGA TACAGCTAGA,

SEQ ID NO: 11: GTCAGTGATA GTCCAAGTTG GC,

SEQ ID NO: 20: CGATTTTGCA GCAGTTTGTA TTAGCCATTG,

SEQ ID NO: 26: GGATGGGAAC AGGTATTTCC ACTCTGATAT GATCAC,

SEQ ID NO: 29: CAGTAATCTA ATTCTCATTA GACTGAGTTT CCTCATTCG,

SEQ ID NO: 31: ACCUCUCAGU ACAGCUACGC G,

SEQ ID NO: 32: CGCGTAGCTG TACTGAGAGG T,

SEQ ID NO: 33: CGCGUAGCUG UACUGAGAGG U,

SEQ ID NO: 37: CGUUAAGCAU CUAGAUUUAA UACCAAACUU ACAAACCCG,

SEQ ID NO: 38: CGGGTTTGTA AGTTTGGTAT TAAATCTAGA TGCTTAACG,

SEQ ID NO: 39: CGGGUUUGUA AGUTUGGUAU UAAAUCUAGA UGCUUAACG,

SEQ ID NO: 40: CCUACUACAC UCUAGGUUUA CAGUUUUUGA UACAGCUAGA,

SEQ ID NO: 41: TCTAGCTGTA TCAAAAACTG TAAACCTAGA GTGTAGTAGG,

SEQ ID NO: 42: UCUAGCUUGUA UCAAAAACUG UAAACCUAGA GUGUAGUAGG,

SEQ ID NO: 43: GUCAGUGAUA GUCCAAGUUG GC,

SEQ ID NO: 44: GCCAACTTGG ACTATCACTG AC,

SEQ ID NO: 45: GCCAACUUGG ACUAUCACUG AC,

SEQ ID NO: 52: CGAUUUUGCA GCAGUUUGUA UUAGCCAUUG,

SEQ ID NO: 53: CAATGGCTAA TACAAACTGC TGCAAAATCG,

SEQ ID NO: 61: CAGUAAUCUA AUUCUCAUUA GACUGAGUU CCUCAUUCG,

SEQ ID NO: 62: CGAATGAGGA AACTCAGTCT AATGAGAATT AGATTACTG,

SEQ ID NO: 63: CGAAUGAGGA AACUCAGUCU AAUGAGAAUU AGAUUACUG,

SEQ ID NO: 109: GGAUGGGAAC AGGUAUUUCC ACUCUGAUAU GAUCAC,

SEQ ID NO: 110: GTGATCATAT CAGAGTGGAA ATACCTGTTC CCATCC, and

SEQ ID NO: 111: GUGAUCAUAU CAGAGUGGAA AUACCUGUUC CCAUCC;

wherein under stringent hybridization assay conditions said hybridization assay probe forms a detectable probe:target hybrid with *Ureaplasma urealyticum* nucleic acid, but does not form a detectable probe:non-target hybrid with nucleic acid from *Mycoplasma genitalium, Mycoplasma hominis* and *Mycoplasma pneumoniae* under said stringent hybridization assay conditions; and

b) a helper probe.

27. The probe mix of claim **26**, wherein said hybridization assay probe comprises a nucleotide base sequence selected from the group consisting of SEQ ID NO: 2, SEQ ID NO: 31, SEQ ID NO: 32, and SEQ ID NO: 33; and said helper probe comprises a nucleotide base sequence selected from the group consisting of:

SEQ ID NO: 1: TCATTGACTT GGTGAGCCAT TACCTCAC,

SEQ ID NO: 3: GCCGTGTCTC AGTCCCATTG TGGCTGTTCT,

SEQ ID NO: 64: UCAUUGACUU GGUGAGCCAU UACCUCAC,

SEQ ID NO: 65: GTGAGGTAAT GGCTCACCAA GTCAATGA,

SEQ ID NO: 66: GUGAGGUAAU GGCUCACCAA GUCAAUGA,

SEQ ID NO: 67: GCCGUGUCUC AGUCCCAUUG UGGCUGUUCU,

SEQ ID NO: 68: AGAACAGCCA CAATGGGACT GAGACACGGC, and

SEQ ID NO: 69: AGAACAGCCA CAAUGGGACU GAGACACGGC.

28. The probe mix of claim **27**, wherein said probe mix is selected from the group consisting of:

(a) a probe mix comprising

a hybridization assay probe consisting of one or more reporter groups and the nucleotide base sequence of either SEQ ID NO: 2 or SEQ ID NO: 31;

a first helper probe consisting of the nucleotide base sequence of either SEQ ID NO: 1 or SEQ ID NO: 64; and

a second helper probe consisting of the nucleotide base sequence of either SEQ ID NO: 3 or SEQ ID NO: 67; and

(b) a probe mix comprising

a hybridization assay probe consisting of one or more reporter groups and the nucleotide base sequence of either SEQ ID NO: 32 or SEQ ID NO: 33;

a first helper probe consisting of the nucleotide base sequence of either SEQ ID NO: 65 or SEQ ID NO: 66; and

a second helper probe consisting of the nucleotide base sequence of either SEQ ID NO: 68 or SEQ ID NO: 69.

29. A probe mix comprising:

a) a hybridization assay probe for detecting Ureaplasma under stringent hybridization assay conditions which is up to 100 nucleotides in length and comprises a nucleotide base sequence selected from the group consisting of SEQ ID NO: 5, SEQ ID NO: 34, SEQ ID NO: 35, and SEQ ID NO: 36; wherein under stringent hybridization assay conditions said hybridization assay probe forms a detectable probe:target hybrid with *Ureaplasma urealyticum* nucleic acid, but does not form a detectable probe:non-target hybrid with nucleic acid from *Mycoplasma genitalium, Mycoplasma hominis* and *Mycoplasma pneumoniae* under said stringent hybridization assay conditions; and

b) a helper probe comprising a nucleotide base sequence selected from the group consisting of:

SEQ ID NO: 4: ATATAAAAGA ACTTTACAAT CTATAAGACC TTCATCGTTC ACGCGGC,

SEQ ID NO: 70: AUAUAAAAGA ACUUUACAAU CUAUAAGACC UUCAUCGUUC ACGCGGC,

SEQ ID NO: 71: GCCGCGTGAA CGATGAAGGT CTTATAGATT GTAAAGTTCT TTTATAT, and

SEQ ID NO: 72: GCCGCGUGAA CGAUGAAGGU CUUAUAGAUU GUAAAGUUCU UUUAUAU.

30. The probe mix of claim **29**, wherein said probe mix is selected from the group consisting of:

(a) a probe mix comprising

a hybridization assay probe consisting of one or more reporter groups and the nucleotide base sequence of either SEQ ID NO: 5 or SEQ ID NO: 34;

a first helper probe consisting of the nucleotide base sequence of either SEQ ID NO: 4 or SEQ ID NO: 70; and

a second helper probe consisting of the nucleotide base sequence of either SEQ ID NO: 6 or SEQ ID NO: 73; and

(b) a probe mix comprising

a hybridization assay probe consisting of one or more reporter groups and the nucleotide base sequence of either SEQ ID NO: 35 or SEQ ID NO: 36;

a first helper probe consisting of the nucleotide base sequence of either SEQ ID NO: 71 or SEQ ID NO: 72; and

a second helper probe consisting of the nucleotide base sequence of either SEQ ID NO: 74 or SEQ ID NO: 75.

31. The probe mix of claim **26**, wherein said hybridization assay probe comprises a nucleotide base sequence selected from the group consisting of SEQ ID NO: 8, SEQ ID NO: 37, SEQ ID NO: 38, and SEQ ID NO: 39; and said helper probe comprises a nucleotide base sequence selected from the group consisting of:

SEQ ID NO: 7: CCTGCGCTCG TTTTACGCCC AGTAAATCCG GATAACGC,

SEQ ID NO: 9: CCTACTACAC TCTAGGTTTA CAGTTTTTGA TACAGCTAGA,

SEQ ID NO: 40: CCUACUACAC UCUAGGUUUA CAGUUUUUGA UACAGCUAGA,

SEQ ID NO: 41: TCTAGCTGTA TCAAAAACTG TAAACCTAGA GTGTAGTAGG,

SEQ ID NO: 42: UCUAGCUGUA UCAAAAACUG UAAACCUAGA GUGUAGUAGG,

SEQ ID NO: 76: CCUGCGCUCG UUUUACGCCC AGUAAAUCCG GAUAACGC,

SEQ ID NO: 77: GCGTTATCCG GATTTACTGG GCG-TAAAACG AGCGCAGG, and

SEQ ID NO: 78: GCGUUAUCCG GAUUUACUGG GCGUAAAACG AGCGCAGG.

32. The probe mix of claim **31**, wherein said probe mix is selected from the group consisting of:

(a) a probe mix comprising

a hybridization assay probe consisting of one or more reporter groups and the nucleotide base sequence of either SEQ ID NO: 8 or SEQ ID NO: 37;

a first helper probe consisting of the nucleotide base sequence of either SEQ ID NO: 7 or SEQ ID NO: 76; and

a second helper probe consisting of the nucleotide base sequence of either SEQ ID NO: 9 or SEQ ID NO: 40; and

(b) a probe mix comprising

a hybridization assay probe consisting of one or more reporter groups and the nucleotide base sequence of either SEQ ID NO: 38 or SEQ ID NO: 39;

a first helper probe consisting of the nucleotide base sequence of either SEQ ID NO: 77 or SEQ ID NO: 78; and

a second helper probe consisting of the nucleotide base sequence of either SEQ ID NO: 41 or SEQ ID NO: 42.

33. The probe mix of claim **26**, wherein said hybridization assay probe comprises a nucleotide base sequence selected from the group consisting of SEQ ID NO: 9, SEQ ID NO: 40, SEQ ID NO: 41, and SEQ ID NO: 42; and said helper probe comprises a nucleotide base sequence selected from the group consisting of:

SEQ ID NO: 8: CGTTAAGCAT CTAGATTTAA TAC-CAAACTT ACAAACCCG,

SEQ ID NO: 10: GCCTTCGCCA CCGGTGTTCT TCCATATATC TA,

SEQ ID NO: 37: CGUUAAGCAU CUAGAUUUAA UACCAAACUU ACAAACCCG,

SEQ ID NO: 38: CGGGTTTGTA AGTTTGGTAT TAAATCTAGA TGCTTAACG,

SEQ ID NO: 39: CGGGUUUGUA AGUUUGGUAU UAAAUCUAGA UGCUUAACG,

SEQ ID NO: 79: GCCUUCGCCA CCGGUGUUCU UCCAUAUAUC UA,

SEQ ID NO: 80: TAGATATATG GAAGAACACC GGTGGCGAAG GC, and

SEQ ID NO: 81: UAGAUAUAUG GAAGAACACC GGUGGCGAAG GC.

34. The probe mix of claim **33**, wherein said probe mix is selected from the group consisting of:

(a) a probe mix comprising

a hybridization assay probe consisting of one or more reporter groups and the nucleotide base sequence of either SEQ ID NO: 9 or SEQ ID NO: 40;

a first helper probe consisting of the nucleotide base sequence of either SEQ ID NO: 8 or SEQ ID NO: 37; and

a second helper probe consisting of the nucleotide base sequence of either SEQ ID NO: 10 or SEQ ID NO: 79; and

(b) a probe mix comprising

a hybridization assay probe consisting of one or more reporter groups and the nucleotide base sequence of either SEQ ID NO: 41 or SEQ ID NO: 42;

a first helper probe consisting of the nucleotide base sequence of either SEQ ID NO: 38 or SEQ ID NO: 39; and

a second helper probe consisting of the nucleotide base sequence of either SEQ ID NO: 80 or SEQ ID NO: 81.

35. The probe mix of claim **26**, wherein said hybridization assay probe comprises a nucleotide base sequence selected from the group consisting of SEQ ID NO: 11, SEQ ID NO: 43, SEQ ID NO: 44, and SEQ ID NO: 45; and said helper probe comprises a nucleotide base sequence selected from the group consisting of:

SEQ ID NO: 10: GCCTTCGCCA CCGGTGTTCT TCCATATATC TA,

SEQ ID NO: 12: CTAATCCTAT TTGCTCCCCA CACTTTCGAG CCTAAGC,

SEQ ID NO: 79: GCCUUCGCCA CCGGUGUUCU UCCAUAUAUC UA,

SEQ ID NO: 80: TAGATATATG GAAGAACACC GGTGGCGAAG GC,

SEQ ID NO: 81: UAGAUAUAUG GAAGAACACC GGUGGCGAAG GC,

SEQ ID NO: 82: CUAAUCCUAU UUGCUCCCCA CACUUUCGAG CCUAAGC,

SEQ ID NO: 83: GCTTAGGCTC GAAAGTGTGG GGAGCAAATA GGATTAG, and

SEQ ID NO: 84: GCUUAGGCUC GAAAGUGUGG GGAGCAAAUA GGAUUAG.

36. The probe mix of claim **35**, wherein said probe mix is selected from the group consisting of:

(a) a probe mix comprising

a hybridization assay probe consisting of one or more reporter groups and the nucleotide base sequence of either SEQ ID NO: 11 or SEQ ID NO: 43;

a first helper probe consisting of the nucleotide base sequence of either SEQ ID NO: 10 or SEQ ID NO: 79; and

a second helper probe consisting of the nucleotide base sequence of either SEQ ID NO: 12 or SEQ ID NO: 82; and

(b) a probe mix comprising

a hybridization assay probe consisting of one or more reporter groups and the nucleotide base sequence of either SEQ ID NO: 44 or SEQ ID NO: 45;

a first helper probe consisting of the nucleotide base sequence of either SEQ ID NO: 80 or SEQ ID NO: 81; and

a second helper probe consisting of the nucleotide base sequence of either SEQ ID NO: 83 or SEQ ID NO: 84.

37. The probe mix of claim **26**, wherein said hybridization assay probe comprises a nucleotide base sequence selected from the group consisting of SEQ ID NO: 20, SEQ ID NO: 52, SEQ ID NO: 53, and SEQ ID NO: 54; and said helper probe comprises a nucleotide base sequence selected from the group consisting of:

SEQ ID NO: 19: TAGCACGTTT GCAGCCCTAG ATATAAGGGG CATGATG,

SEQ ID NO: 21: CGAATTGCAG CCCTCTATCC GAACTGAGAC TAACTTTTTC TG,

SEQ ID NO: 97: UAGCACGUUU GCAGCCCUAG AUAUAAGGGG CAUGAUG,

SEQ ID NO: 98: CATCATGCCC CTTATATCTA GGGCTGCAAA CGTGCTA,

SEQ ID NO: 99: CAUCAUGCCC CUUAUAUCUA GGGCUGCAAA CGUGCUA,

SEQ ID NO: 100: CGAAUUGCAG CCCUCUAUCC GAACUGAGAC UAACUUUUUC UG,

SEQ ID NO: 101: CAGAAAAAGT TAGTCTCAGT TCGGATAGAG GGCTGCAATT CG, and,

SEQ ID NO: 102: CAGAAAAAGU UAGUCUCAGU UCGGAUAGAG GGCUGCAAUU CG.

38. The probe mix of claim wherein **37**, said probe mix is selected from the group consisting of:

(a) a probe mix comprising

a hybridization assay probe consisting of one or more reporter groups and the nucleotide base sequence of either SEQ ID NO: 20 or SEQ ID NO: 52;

a first helper probe consisting of the nucleotide base sequence of either SEQ ID NO: 19 or SEQ ID NO: 97; and

a second helper probe consisting of the nucleotide base sequence of either SEQ ID NO: 21 or SEQ ID NO: 100; and

(b) a probe mix comprising

a hybridization assay probe consisting of one or more reporter groups and the nucleotide base sequence of either SEQ ID NO: 53 or SEQ ID NO: 54;

a first helper probe consisting of the nucleotide base sequence of either SEQ ID NO: 98 or SEQ ID NO: 99; and

a second helper probe consisting of the nucleotide base sequence of either SEQ ID NO: 101 or SEQ ID NO: 102.

39. The probe mix of claim **26**, wherein said hybridization assay probe comprises a nucleotide base sequence selected from the group consisting of SEQ ID NO: 29, SEQ ID NO: 61, SEQ ID NO: 62, and SEQ ID NO: 63; and said helper probe comprises a nucleotide base sequence selected from the group consisting of:

SEQ ID NO: 28: GAGATCAACG GATTAAAGCC TCT-TATCAGC TACCCGTTGC TTATCGCAGA TTAGCACG,

SEQ ID NO: 30: CACTTCACCA GGTATCGCTC TGT-TAAACTA TGAATTCATT TATA,

SEQ ID NO: 115: GAGAUCAACG GAUUAAAGCC UCUUAUCAGC UACCCGUUGC UUAUCGCAGA UUAGCACG,

SEQ ID NO: 116: CGTGCTAATC TGCGATAAGC AACGGGTAGC TGATAAGAGG CTTTAATCCG TTGATCTC,

SEQ ID NO: 117: CGUGCUAAUC UGCGAUAAGC AACGGGUAGC UGAUAAGAGG CUUUAAUCCG UUGAUCUC,

SEQ ID NO: 118: CACUUCACCA GGUAUCGCUC UGUUAAACUA UGAAUUCAUU UAUA,

SEQ ID NO: 119: TATAAATGAA TTCATAGTTT AACAGAGCGA TACCTGGTGA AGTG, and

SEQ ID NO: 120: UAUAAAUGAA UUCAUAGUUU AACAGAGCGA UACCUGGUGA AGUG.

40. The probe mix of claim **39**, wherein said probe mix is selected from the group consisting of:

(a) a probe mix comprising

a hybridization assay probe consisting of one or more reporter groups and the nucleotide base sequence of either SEQ ID NO: 29 or SEQ ID NO: 61;

a first helper probe consisting of the nucleotide base sequence of either SEQ ID NO: 28 or SEQ ID NO: 115; and

a second helper probe consisting of the nucleotide base sequence of either SEQ ID NO: 30 or SEQ ID NO: 118; and

(a) a probe mix comprising

a hybridization assay probe consisting of one or more reporter groups and the nucleotide base sequence of either SEQ ID NO: 62 or SEQ ID NO: 63;

a first helper probe consisting of the nucleotide base sequence of either SEQ ID NO: 116 or SEQ ID NO: 117; and

a second helper probe consisting of the nucleotide base sequence of either SEQ ID NO: 119 or SEQ ID NO: 120.

41. A probe mix comprising

a hybridization assay probe 18 to 100 nucleotides in length comprising a nucleotide base sequence selected from the group consisting of:

SEQ ID NO: 121: CAACACCGAC TCGTTCGAGC,

SEQ ID NO: 122: CAACACCGAC CCATTCGG,

SEQ ID NO: 126: CAACACCGAC UCGUUCGAGC,

SEQ ID NO: 127: CAACACCGAC CCAUUCGG,

SEQ ID NO: 131: GCTCGAACGA GTCGGTGTTG,

SEQ ID NO: 132: CCGAATGGGT CGGTGTTG,

SEQ ID NO: 136: GCUCGAACGA GUCGGUGUUG, and

SEQ ID NO: 137: CCGAAUGGGU CGGUGUUG;

provided that said hybridization assay probe forms a detectable probe:target hybrid under stringent hybridization assay conditions with either *Ureaplasma urealyticum* biotype 1 nucleic acid or *Ureaplasma urealyticum* biotype 2 nucleic acid, wherein said hybridization assay probe does not form said detectable probe:target hybrid with both *Ureaplasma urealyticum* biotype 1 nucleic acid and *Ureaplasma urealyticum* biotype 2 nucleic acid under said stringent hybridization assay conditions,

further provided that said hybridization assay probe does not hybridize to nucleic acid from *Mycoplasma genitalium, Mycoplasma hominis* and *Mycoplasma pneumoniae* to form a detectable probe:non-target hybrid under said stringent hybridization assay conditions; and

a helper probe comprising a nucleotide base sequence selected from the group consisting of:

SEQ ID NO: 123: CGACATTTAA TGATGATCGT TTACGGTGTG GAC,

SEQ ID NO: 124: GCCGACATTT AATGATGATC GTTTACGGTG TGGAC,

SEQ ID NO: 125: CCCAGGCACA TCATTTAATG CGTTAGCTA,

SEQ ID NO: 128: CGACAUUUAA UGAUGAUCGU UUACGGUGUG GAC,

SEQ ID NO: 129: GCCGACAUUU AAUGAUGAUC GUUUACGGUG UGGAC,

SEQ ID NO: 130: CCCAGGCACA UCAUUUAAUG CGUUAGCUA,

SEQ ID NO: 133: GTCCACACCG TAAACGATCA TCATTAAATG TCG,

SEQ ID NO: 134: GTCCACACCG TAAACGATCA TCATTAAATG TCGGC,

SEQ ID NO: 135: TAGCTAACGC ATTAAATGAT GTGCCTGGG,

SEQ ID NO: 138: GUCCACACCG UAAACGAUCA UCAUUAAAUG UCG,

SEQ ID NO: 139: GUCCACACCG UAAACGAUCA UCAUUAAAUG UCGGC, and

SEQ ID NO: 140: UAGCUAACGC AUUAAAUGAU GUGCCUGGG.

42. The probe mix of claim **41**, wherein said probe mix is selected from the group consisting of:

(a) a probe mix comprising

a hybridization assay probe consisting of one or more reporter groups and the nucleotide base sequence of either SEQ ID NO: 121 or SEQ ID NO: 126,

a first helper probe consisting of the nucleotide base sequence of either SEQ ID NO: 123 or SEQ ID NO: 128; and

a second helper probe consisting of the nucleotide base sequence of either SEQ ID NO: 125 or SEQ ID NO: 130; and

(b) a probe mix comprising

a hybridization assay probe consisting of one or more reporter groups and the nucleotide base sequence of either SEQ ID NO: 131 or SEQ ID NO: 136;

a first helper probe consisting of the nucleotide base sequence of either SEQ ID NO: 133 or SEQ ID NO: 138; and

a second helper probe consisting of the nucleotide base sequence of either SEQ ID NO: 135 or SEQ ID NO: 140.

43. A probe mix selected from the group consisting of:

(a) a probe mix comprising

a hybridization assay probe consisting of one or more reporter groups and the nucleotide base sequence of either SEQ ID NO: 122 or SEQ ID NO: 127,

a first helper probe consisting of the nucleotide base sequence of either SEQ ID NO: 124 or SEQ ID NO: 129; and

a second helper probe consisting of the nucleotide base sequence of either SEQ ID NO: 125 or SEQ ID NO: 130; and

(b) a probe mix comprising

a hybridization assay probe consisting of one or more reporter groups and the nucleotide base sequence of either SEQ ID NO: 132 or SEQ ID NO: 137;

a first helper probe consisting of the nucleotide base sequence of either SEQ ID NO: 134 or SEQ ID NO: 139; and

a second helper probe consisting of the nucleotide base sequence of either SEQ ID NO: 135 or SEQ ID NO: 140.

44. A probe mix comprising

a) a hybridization assay probe for detecting *Ureaplasma urealyticum* under stringent hybridization assay conditions which is 28 to 100 nucleotides in length and comprises a nucleotide base sequence selected from the group consisting of:

SEQ ID NO: 14: CGTTCGAGCC GACATTTAAT GATGATCG,

SEQ ID NO: 46: CGUUCGAGCC GACAUUUAAU GAUGAUCG,

SEQ ID NO: 47: CGATCATCAT TAAATGTCGG CTCGAACG, and

SEQ ID NO: 48: CGAUCAUCAU UAAAUGUCGG CUCGAACG;

wherein under said stringent hybridization assay conditions said hybridization assay probe forms a detectable probe:target hybrid with *Ureaplasma urealyticum* nucleic acid, but does not form a detectable probe:non-target hybrid with nucleic acid from *Mycoplasma genitalium, Mycoplasma hominis* and *Mycoplasma pneumoniae* under said stringent hybridization assay conditions; and

b) a helper probe consisting of a nucleotide base sequence selected from the group consisting of:

SEQ ID NO: 13: TTTACGGTGT GGACTACTAG GGTAT,

SEQ ID NO: 15: GCGTTAGCTA CAACACCGAC T,

SEQ ID NO: 85: UUUACGGUGU GGACUACUAG GGUAU,

SEQ ID NO: 86: ATACCCTAGT AGTCCACACC GTAAA,

SEQ ID NO: 87: AUACCCUAGU AGUCCACACC GUAAA,

SEQ ID NO: 88: GCGUUAGCUA CAACACCGAC U,

SEQ ID NO: 89: AGTCGGTGTT GTAGCTAACG C, and

SEQ ID NO: 90: AGUCGGUGUU GUAGCUAACG C.

45. The probe mix of claim **44**, wherein said probe mix is selected from the group consisting of:

(a) a probe mix comprising

a hybridization assay probe consisting of one or more reporter groups and the nucleotide base sequence of either SEQ ID NO: 14 or SEQ ID NO: 46;

a first helper probe consisting of the nucleotide base sequence of either SEQ ID NO: 13 or SEQ ID NO: 85; and

a second helper probe consisting of the nucleotide base sequence of either SEQ ID NO: 15 or SEQ ID NO: 88; and

(b) a probe mix comprising

a hybridization assay probe consisting of one or more reporter groups and the nucleotide base sequence of either SEQ ID NO: 47 or SEQ ID NO: 48;

a first helper probe consisting of the nucleotide base sequence of either SEQ ID NO: 86 or SEQ ID NO: 87; and

a second helper probe consisting of the nucleotide base sequence of either SEQ ID NO: 89 or SEQ ID NO: 90.

46. A probe mix comprising

a) a hybridization assay probe for detecting *Ureaplasma urealyticum* under stringent hybridization assay conditions which is 24 to 100 nucleotides in length and comprises a nucleotide base sequence selected from the group consisting of:

SEQ ID NO: 17: GCGTCGCAAT AGATGTCAAA CCTAG,

SEQ ID NO: 49: GCGUCGCAAU AGAUGUCAAA CCUAG,

SEQ ID NO: 50: CTAGGTTTGA CATCTATTGC GACGC, and

SEQ ID NO: 51: CUAGGUUUGA CAUCUAUUGC GACGC;

wherein under said stringent hybridization assay conditions said hybridization assay probe forms a detectable probe:target hybrid with a *Ureaplasma urealyticum* target nucleic acid, but does not form a detectable probe:non-target hybrid with nucleic acid from *Mycoplasma genitalium, Mycoplasma hominis* and *Mycoplasma pneumoniae* under said stringent hybridization assay conditions; and

b) a helper probe consisting of a nucleotide base sequence selected from the group consisting of:

SEQ ID NO: 16: GTAAGGTTCT ACGTGTATTG TCAAATTAAG CAACATGCTC CACCAC,

SEQ ID NO: 18: CGACAACCAT GCACCACCTG TCATATTGTT AACCTCAAC,

SEQ ID NO: 91: GUAAGGUUCU ACGUGUAUUG UCAAAUUAAG CAACAUGCUC CACCAC,

SEQ ID NO: 92: GTGGTGGAGC ATGTTGCTTA ATTTGACAAT ACACGTAGAA CCTTAC,

SEQ ID NO: 93: GUGGUGGAGC AUGUUGCUUA AUUUGACAAU ACACGUAGAA CCUUAC,

SEQ ID NO: 94: CGACAACCAU GCACCACCUG UCAUAUUGUU AACCUCAAC,

SEQ ID NO: 95: GTTGAGGTTA ACAATATGAC AGGTGGTGCA TGGTTGTCG, and

SEQ ID NO: 96: GUUGAGGUUA ACAAUAUGAC AGGUGGUGCA UGGUUGUCG.

47. The probe mix of claim **46**, wherein said probe mix is selected from the group consisting of:

(a) a probe mix comprising

a hybridization assay probe consisting of one or more reporter groups and the nucleotide base sequence of either SEQ ID NO: 17 or SEQ ID NO: 49;

a first helper probe consisting of the nucleotide base sequence of either SEQ ID NO: 16 or SEQ ID NO: 91; and

a second helper probe consisting of the nucleotide base sequence of either SEQ ID NO: 18 or SEQ ID NO: 94; and

(b) a probe mix comprising

a hybridization assay probe consisting of one or more reporter groups and the nucleotide base sequence of either SEQ ID NO: 50 or SEQ ID NO: 51;

a first helper probe consisting of the nucleotide base sequence of either SEQ ID NO: 92 or SEQ ID NO: 93; and

a second helper probe consisting of the nucleotide base sequence of either SEQ ID NO: 95 or SEQ ID NO: 96.

48. A method for detecting the presence of Ureaplasma in a sample and distinguishing said Ureaplasma from *Mycoplasma genitalium, Mycoplasma pneumoniae,* and *Mycoplasma hominis* comprising the steps of:

a) providing to said sample a hybridization assay probe comprising an oligonucleotide which under stringent hybridization assay conditions hybridizes to a *Ureaplasma urealyticum* target nucleic acid selected from the group consisting of

SEQ ID NO: 31: ACCUCUCAGU ACAGCUACGC G,

SEQ ID NO: 33: CGCGUAGCUG UACUGAGAGG U,

SEQ ID NO: 37: CGUUAAGCAU CUAGAUUUAA UACCAAACUU ACAAACCCG,

SEQ ID NO: 39: CGGGUUUGUA AGUUUGGUAU UAAAUCUAGA UGCUUAACG,

SEQ ID NO: 40: CCUACUACAC UCUAGGUUUA CAGUUUUUGA UACAGCUAGA,

SEQ ID NO: 42: UCUAGCUGUA UCAAAAACUG UAAACCUAGA GUGUAGUAGG,

SEQ ID NO: 43: GUCAGUGAUA GUCCAAGUUG GC,

SEQ ID NO: 45: GCCAACUUGG ACUAUCACUG AC,

SEQ ID NO: 52: CGAUUUUGCA GCAGUUUGUA UUAGCCAUUG,

SEQ ID NO: 54: CAAUGGCUAA UACAAACUGC UGCAAAAUCG,

SEQ ID NO: 55: GCUAUUUUCG GCUCUAGAGU GCUUGACUUC UGUGUUCGGG AUG,

SEQ ID NO: 57: CAUCCCGAAC ACAGAAGUCA AGCACUCUAG AGCCGAAAAU AGC,

SEQ ID NO: 58: CGGCUCUAGA GUGCUUGACU UCUGUGUUCG,

SEQ ID NO: 60: CGAACACAGA AGUCAAGCAC UCUAGAGCCG,

SEQ ID NO: 61: CAGUAAUCUA AUUCUCAUUA GACUGAGUUU CCUCAUUCG,

SEQ ID NO: 63: CGAAUGAGGA AACUCAGUCU AAUGAGAAUU AGAUUACUG,

SEQ ID NO: 109: GGAUGGGAAC AGGUAUUUCC ACUCUGAUAU GAUCAC, and

SEQ ID NO: 111: GUGAUCAUAU CAGAGUGGAA AUACCUGUUC CCAUCC;

wherein under said stringent hybridization assay conditions said oligonucleotide hybridizes with said target nucleic acid to form a detectable probe:target hybrid and does not hybridize to form a detectable probe:non-target hybrid with *Mycoplasma genitalium, Mycoplasma hominis* and *Mycoplasma pneumoniae* nucleic acid under said stringent hybridization assay conditions; and

b) employing said stringent hybridization assay conditions and detecting the presence of said detectable probe:target hybrid formed under said stringent hybridization assay conditions as an indication that Ureaplasma may be present in said sample.

49. The method of claim **48**, wherein target nucleic acid is selected from the group consisting of SEQ ID NO: 31 and SEQ ID NO: 33.

50. The method of claim **48**, wherein said target nucleic acid is selected from the group consisting of SEQ ID NO: 37 and SEQ ID NO: 39.

51. The method of claim **48**, wherein said target nucleic acid is selected from the group consisting of SEQ ID NO: 40 and SEQ ID NO: 42.

52. The method of claim **48**, wherein said target nucleic acid is selected from the group consisting of SEQ ID NO: 43 and SEQ ID NO: 45.

53. The method of claim 48, wherein said target nucleic acid is selected from the group consisting of SEQ ID NO: 52 and SEQ ID NO: 54.

54. The method of claim 48, wherein said target nucleic acid is selected from the group consisting of SEQ ID NO: 55 and SEQ ID NO: 57.

55. The method of claim 48, wherein said target nucleic acid is selected from the group consisting of SEQ ID NO: 58 and SEQ ID NO: 60.

56. The method of claim 48, wherein said target nucleic acid is selected from the group consisting of SEQ ID NO: 61 and SEQ ID NO: 63.

57. The method of claim 48, wherein said target nucleic acid is selected from the group consisting of SEQ ID NO: 109 and SEQ ID NO: 111.

58. A method for detecting the presence of Ureaplasma in a sample and distinguishing said Ureaplasma from *Mycoplasma genitalium, Mycoplasma pneumoniae,* and *Mycoplasma hominis,* comprising the steps of:

a) providing to said sample a hybridization assay probe comprising a detection nucleotide base sequence selected from the group consisting of:

SEQ ID NO: 2: ACCTCTCAGT ACAGCTACGC G,

SEQ ID NO: 8: CGTTAAGCAT CTAGATTTAA TACCAAACTT ACAAACCCG,

SEQ ID NO: 9: CCTACTACAC TCTAGGTTTA CAGTTTTTGA TACAGCTAGA,

SEQ ID NO: 11: GTCAGTGATA GTCCAAGTTG GC,

SEQ ID NO: 20: CGATTTTGCA GCAGTTTGTA TTAGCCATTG,

SEQ ID NO: 22: GCTATTTTCG GCTCTAGAGT GCTTGACTTC TGTGTTCGGG ATG,

SEQ ID NO: 23: CGGCTCTAGA GTGCTTGACT TCTGTGTTCG,

SEQ ID NO: 26: GGATGGGAAC AGGTATTTCC ACTCTGATAT GATCAC,

SEQ ID NO: 29: CAGTAATCTA ATTCTCATTA GACTGAGTTT CCTCATTCG,

SEQ ID NO: 31: ACCUCUCAGU ACAGCUACGC G,

SEQ ID NO: 32: CGCGTAGCTG TACTGAGAGG T,

SEQ ID NO: 33: CGCGUAGCUG UACUGAGAGG U,

SEQ ID NO: 37: CGUUAAGCAU CUAGAUUUAA UACCAAACUU ACAAACCCG,

SEQ ID NO: 38: CGGGTTTGTA AGTTTGGTAT TAAATCTAGA TGCTTAACG,

SEQ ID NO: 39: CGGGUUUGUA AGUUUGGUAU UAAAUCUAGA UGCUUAACG,

SEQ ID NO: 40: CCUACUACAC UCUAGGUUUA CAGUUUUUGA UACAGCUAGA,

SEQ ID NO: 41: TCTAGCTGTA TCAAAAACTG TAAACCTAGA GTGTAGTAGG,

SEQ ID NO: 42: UCUAGCUGUA UCAAAAACUG UAAACCUAGA GUGUAGUAGG,

SEQ ID NO: 43: GUCAGUGAUA GUCCAAGUUG GC,

SEQ ID NO: 44: GCCAACTTGG ACTATCACTG AC,

SEQ ID NO: 45: GCCAACUUGG ACUAUCACUG AC,

SEQ ID NO: 52: CGAUUUUGCA GCAGUUUGUA UUAGCCAUUG,

SEQ ID NO: 53: CAATGGCTAA TACAAACTGC TGCAAAATCG,

SEQ ID NO: 54: CAAUGGCUAA UACAAACUGC UGCAAAAUCG,

SEQ ID NO: 55: GCUAUUUUCG GCUCUAGAGU GCUUGACUUC UGUGUUCGGG AUG,

SEQ ID NO: 56: CATCCCGAAC ACAGAAGTCA AGCACTCTAG AGCCGAAAAT AGC,

SEQ ID NO: 57: CAUCCCGAAC ACAGAAGUCA AGCACUCUAG AGCCGAAAAU AGC,

SEQ ID NO: 58: CGGCUCUAGA GUGCUUGACU UCUGUGUUCG,

SEQ ID NO: 59: CGAACACAGA AGTCAAGCAC TCTAGAGCCG,

SEQ ID NO: 60: CGAACACAGA AGUCAAGCAC UCUAGAGCCG,

SEQ ID NO: 61: CAGUAAUCUA AUUCUCAUUA GACUGAGUUU CCUCAUUCG,

SEQ ID NO: 62: CGAATGAGGA AACTCAGTCT AATGAGAATT AGATTACTG,

SEQ ID NO: 63: CGAAUGAGGA AACUCAGUCU AAUGAGAAUU AGAUUACUG,

SEQ ID NO: 109: GGAUGGGAAC AGGUAUUUCC ACUCUGAUAU GAUCAC,

SEQ ID NO: 110: GTGATCATAT CAGAGTGGAA ATACCTGTTC CCATCC, and

SEQ ID NO: 111: GUGAUCAUAU CAGAGUGGAA AUACCUGUUC CCAUCC;

wherein under stringent hybridization assay conditions said hybridization assay probe hybridizes with nucleic acid from *Ureaplasma urealyticum* to form a probe:target hybrid and does not hybridize to nucleic acid from *Mycoplasma genitalium, Mycoplasma hominis* and *Mycoplasma pneumoniae* to form a detectable probe:non-target hybrid; and

b) employing said stringent hybridization assay conditions and detecting the presence of said detectable probe:target hybrid formed under said stringent hybridization assay conditions as an indication that Ureaplasma may be present in said sample.

59. The method of claim 58, wherein said hybridization assay probe comprises a detection nucleotide base sequence selected from the group consisting of SEQ ID NO: 2, SEQ ID NO: 31, SEQ ID NO: 32, and SEQ ID NO: 33.

60. The method of claim 59, wherein said method uses one or more helper probes consisting of a nucleotide base sequence selected from the group consisting of:

SEQ ID NO: 1: TCATTGACTT GGTGAGCCAT TACCTCAC,

SEQ ID NO: 3: GCCGTGTCTC AGTCCCATTG TGGCTGTTCT,

SEQ ID NO: 64: UCAUUGACUU GGUGAGCCAU UACCUCAC,

SEQ ID NO: 65: GTGAGGTAAT GGCTCACCAA GTCAATGA,

SEQ ID NO: 66: GUGAGGUAAU GGCUCACCAA GUCAAUGA,

SEQ ID NO: 67: GCCGUGUCUC AGUCCCAUUG UGGCUGUUCU,

SEQ ID NO: 68: AGAACAGCCA CAATGGGACT GAGACACGGC, and

SEQ ID NO: 69: AGAACAGCCA CAAUGGGACU GAGACACGGC.

61. A method for detecting the presence of Ureaplasma in a sample and distinguishing said Ureaplasma from *Mycoplasma genitalium, Mycoplasma pneumoniae,* and *Mycoplasma hominis,* comprising the steps of:

a) providing to said sample a hybridization assay probe comprising a detection nucleotide base sequence

selected from the group consisting of: SEQ ID NO: 5, SEQ ID NO: 34, SEQ ID NO: 35, and SEQ ID NO: 36;

wherein under stringent hybridization assay conditions said hybridization assay probe hybridizes with nucleic acid from *Ureaplasma urealyticum* to form a probe:target hybrid and does not hybridize to nucleic acid from *Mycoplasma genitalium, Mycoplasma hominis* and *Mycoplasma pneumoniae* to form a detectable probe:non-target hybrid; and

b) employing said stringent hybridization assay conditions and detecting the presence of said detectable probe:target hybrid formed under said stringent hybridization assay conditions as an indication that Ureaplasma may be present in said sample;

wherein said method uses one or more helper probes consisting of a nucleotide base sequence selected from the group consisting of:

SEQ ID NO: 4: ATATAAAAGA ACTTTACAAT CTATAAGACC TTCATCGTTC ACGCGGC,

SEQ ID NO: 6: GGCACATAGT TAGCCGATAC TTATTCAAAT GGTACAGTCA AA,

SEQ ID NO: 70: AUAUAAAAGA ACUUUACAAU CUAUAAGACC UUCAUCGUUC ACGCGGC,

SEQ ID NO: 71: GCCGCGTGAA CGATGAAGGT CTTATAGATT GTAAAGTTCT TTTATAT,

SEQ ID NO: 72: GCCGCGUGAA CGAUGAAGGU CUUAUAGAUU GUAAAGUUCU UUUAUAU,

SEQ ID NO: 73: GGCACAUAGU UAGCCGAUAC UUAUUCAAAU GGUACAGUCA AA,

SEQ ID NO: 74: TTTGACTGTA CCATTTGAAT AAGTATCGGC TAACTATGTG CC, and

SEQ ID NO: 75: UUUGACUGUA CCAUUUGAAU AAGUAUCGGC UAACUAUGUG CC.

62. The method of claim **58**, wherein said hybridization assay probe comprises a detection nucleotide base sequence selected from the group consisting of SEQ ID NO: 8, SEQ ID NO: 37, SEQ ID NO: 38, and SEQ ID NO: 39.

63. The method of claim **62**, wherein said method uses one or more helper probes consisting of a nucleotide base sequence selected from the group consisting of:

SEQ ID NO: 7: CCTGCGCTCG TTTTACGCCC AGTAAATCCG GATAACGC,

SEQ ID NO: 9: CCTACTACAC TCTAGGTTTA CAGTTTTTGA TACAGCTAGA,

SEQ ID NO: 40: CCUACUACAC UCUAGGUUUA CAGUUUUUGA UACAGCUAGA,

SEQ ID NO: 41: TCTAGCTGTA TCAAAAACTG TAAACCTAGA GTGTAGTAGG,

SEQ ID NO: 42: UCUAGCUGUA UCAAAAACUG UAAACCUAGA GUGUAGUAGG,

SEQ ID NO: 76: CCUGCGCUCG UUUUACGCCC AGUAAAUCCG GAUAACGC,

SEQ ID NO: 77: GCGTTATCCG GATTTACTGG GCGTAAAACG AGCGCAGG, and

SEQ ID NO: 78: GCGUUAUCCG GAUUUACUGG GCGUAAAACG AGCGCAGG.

64. The method of claim **58**, wherein said hybridization assay probe comprises a detection nucleotide base sequence selected from the group consisting of SEQ ID NO: 9, SEQ ID NO: 40, SEQ ID NO: 41, and SEQ ID NO: 42.

65. The method of claim **64**, wherein said method uses one or more helper probes consisting of a nucleotide base sequence selected from the group consisting of:

SEQ ID NO: 8: CGTTAAGCAT CTAGATTTAA TACCAAACTT ACAAACCCG,

SEQ ID NO: 10: GCCTTCGCCA CCGGTGTTCT TCCATATATC TA,

SEQ ID NO: 37: CGUUAAGCAU CUAGAUUUAA UACCAAACUU ACAAACCCG,

SEQ ID NO: 38: CGGGTTTGTA AGTTTGGTAT TAAATCTAGA TGCTTAACG,

SEQ ID NO: 39: CGGGUUUGUA AGUUUGGUAU UAAAUCUAGA UGCUUAACG,

SEQ ID NO: 79: GCCUUCGCCA CCGGUGUUCU UCCAUAUAUC UA,

SEQ ID NO: 80: TAGATATATG GAAGAACACC GGTGGCGAAG GC, and

SEQ ID NO: 81: UAGAUAUAUG GAAGAACACC GGUGGCGAAG GC.

66. The method of claim **58**, wherein said hybridization assay probe comprises a detection nucleotide base sequence selected from the group consisting of SEQ ID NO: 11, SEQ ID NO: 43, SEQ ID NO: 44, and SEQ ID NO: 45.

67. The method of claim **66**, wherein said method uses one or more helper probes consisting of a nucleotide base sequence selected from the group consisting of:

SEQ ID NO: 10: GCCTTCGCCA CCGGTGTTCT TCCATATATC TA,

SEQ ID NO: 12: CTAATCCTAT TTGCTCCCCA CACTTTCGAG CCTAAGC,

SEQ ID NO: 79: GCCUUCGCCA CCGGUGUUCU UCCAUAUAUC UA,

SEQ ID NO: 80: TAGATATATG GAAGAACACC GGTGGCGAAG GC,

SEQ ID NO: 81: UAGAUAUAUG GAAGAACACC GGUGGCGAAG GC,

SEQ ID NO: 82: CUAAUCCUAU UUGCUCCCCA CACUUUCGAG CCUAAGC,

SEQ ID NO: 83: GCTTAGGCTC GAAAGTGTGG GGAGCAAATA GGATTAG, and

SEQ ID NO: 84: GCUUAGGCUC GAAAGUGUGG GGAGCAAAUA GGAUUAG.

68. The method of claim **58**, wherein said hybridization assay probe comprises a detection nucleotide base sequence selected from the group consisting of SEQ ID NO: 20, SEQ ID NO: 52, SEQ ID NO: 53, and SEQ ID NO: 54.

69. The method of claim **68**, wherein said method uses one or more helper probes consisting of a nucleotide base sequence selected from the group consisting of:

SEQ ID NO: 19: TAGCACGTTT GCAGCCCTAG ATATAAGGGG CATGATG,

SEQ ID NO: 21: CGAATTGCAG CCCTCTATCC GAACTGAGAC TAACTTTTTC TG,

SEQ ID NO: 97: UAGCACGUUU GCAGCCCUAG AUAUAAGGGG CAUGAUG,

SEQ ID NO: 98: CATCATGCCC CTTATATCTA GGGCTGCAAA CGTGCTA,

SEQ ID NO: 99: CAUCAUGCCC CUUAUAUCUA GGGCUGCAAA CGUGCUA,

SEQ ID NO: 100: CGAAUUGCAG CCCUCUAUCC GAACUGAGAC UAACUUUUUC UG,

SEQ ID NO: 101: CAGAAAAAGT TAGTCTCAGT TCGGATAGAG GGCTGCAATT CG, and,

SEQ ID NO: 102: CAGAAAAAGU UAGUCUCAGU UCGGAUAGAG GGCUGCAAUU CG.

70. The method of claim **58**, wherein said hybridization assay probe comprises a detection nucleotide base sequence selected from the group consisting of SEQ ID NO: 22, SEQ ID NO: 55, SEQ ID NO: 56, and SEQ ID NO: 57.

71. The method of claim 70, wherein said method uses one or more helper probes consisting of a nucleotide base sequence selected from the group consisting of:

SEQ ID NO: 24: GGAACAGGTA TTTCCACTCT GATATGATCA CTAC,

SEQ ID NO: 25: GCGTAGCGAT GACCTATTTT ACTTGC,

SEQ ID NO: 103: GGAACAGGUA UUUCCACUCU GAUAUGAUCA CUAC,

SEQ ID NO: 104: GTAGTGATCA TATCAGAGTG GAAATACCTG TTCC,

SEQ ID NO: 105: GUAGUGAUCA UAUCAGAGUG GAAAUACCUG UUCC,

SEQ ID NO: 106: GCGUAGCGAU GACCUAUUUU ACUUGC,

SEQ ID NO: 107: GCAAGTAAAA TAGGTCATCG CTACGC, and

SEQ ID NO: 108: GCAAGUAAAA UAGGUCAUCG CUACGC.

72. The method of claim 58, wherein said hybridization assay probe comprises a detection nucleotide base sequence selected from the group consisting of SEQ ID NO: 23, SEQ ID NO: 58, SEQ ID NO: 59, and SEQ ID NO: 60.

73. The method of claim 72, wherein said method uses one or more helper probes consisting of a nucleotide base sequence selected from the group consisting of:

SEQ ID NO: 26: GGATGGGAAC AGGTATTTCC ACTCTGATAT GATCAC,

SEQ ID NO: 27: GCGTAGCGAT GACCTATTTT ACTTGCGCTA TTTT,

SEQ ID NO: 109: GGAUGGGAAC AGGUAUUCC ACUCUGAUAU GAUCAC,

SEQ ID NO: 110: GTGATCATAT CAGAGTGGAA ATACCTGTTC CCATCC,

SEQ ID NO: 111: GUGAUCAUAU CAGAGUGGAA AUACCUGUUC CCAUCC,

SEQ ID NO: 112: GCGUAGCGAU GACCUAUUUU ACUUGCGCUA UUUU,

SEQ ID NO: 113: AAAATAGCGC AAGTAAAATA GGTCATCGCT ACGC, and

SEQ ID NO: 114: AAAAUAGCGC AAGUAAAAUA GGUCAUCGCU ACGC.

74. The method of claim 58, wherein said hybridization assay probe comprises a detection nucleotide base sequence selected from the group consisting of SEQ ID NO: 29, SEQ ID NO: 61, SEQ ID NO: 62, and SEQ ID NO: 63.

75. The method of claim 74, wherein said method uses one or more helper probes consisting of a nucleotide base sequence selected from the group consisting of:

SEQ ID NO: 28: GAGATCAACG GATTAAAGCC TCTTATCAGC TACCCGTTGC TTATCGCAGA TTAGCACG,

SEQ ID NO: 30: CACTTCACCA GGTATCGCTC TGTTAAACTA TGAATTCATT TATA,

SEQ ID NO: 115: GAGAUCAACG GAUUAAGCC UCUUAUCAGC UACCCGUUGC UUAUCGCAGA UUAGCACG,

SEQ ID NO: 116: CGTGCTAATC TGCGATAAGC AACGGGTAGC TGATAAGAGG CTTTAATCCG TTGATCTC,

SEQ ID NO: 117: CGUGCUAAUC UGCGAUAAGC AACGGGUAGC UGAUAAGAGG CUUUAAUCCG UUGAUCUC,

SEQ ID NO: 118: CACUUCACCA GGUAUCGCUC UGUUAAACUA UGAAUUCAUU UAUA,

SEQ ID NO: 119: TATAAATGAA TTCATAGTTT AACAGAGCGA TACCTGGTGA AGTG, and

SEQ ID NO: 120: UAUAAAUGAA UUCAUAGUUU AACAGAGCGA UACCUGGUGA AGUG.

76. The method of claim 58, wherein said hybridization assay probe comprises a detection nucleotide base sequence selected from the group consisting of SEQ ID NO: 26, SEQ ID NO: 109, SEQ ID NO: 110, and SEQ ID NO: 111.

77. The method of any one of claims 59, 60, and 61–76, wherein said hybridization assay probe consists of said detection nucleotide base sequence and one or more reporter groups.

78. A method for specifically detecting the presence of *Ureaplasma urealyticum* biotype 1 or *Ureaplasma urealyticum* biotype 2 comprising the steps of:

a) contacting a sample with a hybridization assay probe able to hybridize under stringent hybridization assay conditions to a *Ureaplasma urealyticum* biotype specific target nucleic acid sequence to form a probe:target hybrid with either *Ureaplasma urealyticum* biotype 1 or *Ureaplasma urealyticum* biotype 2 nucleic acid, wherein said hybridization assay probe does not hybridize to nucleic acid from both *Ureaplasma urealyticum* biotype 1 and *Ureaplasma urealyticum* biotype 2 under said stringent hybridization assay conditions to form a detectable probe:non-target hybrid, said *Ureaplasma urealyticum* biotype specific target nucleic acid sequence being selected from the group consisting of:

SEQ ID NO: 126: CAACACCGAC UCGUUCGAGC,

SEQ ID NO: 127: CAACACCGAC CCAUUCGG,

SEQ ID NO: 136: GCUCGAACGA GUCGGUGUUG, and

SEQ ID NO: 137: CCGAAUGGGU CGGUGUUG;

provided that under said stringent hybridization conditions said probe does not hybridize to nucleic acid from *Mycoplasma genitalium, Mycoplasma hominis* and *Mycoplasma pneumoniae* to form a detectable probe:non-target hybrid; and

b) employing said stringent hybridization assay conditions and detecting the presence of said detectable probe:target hybrid formed under said stringent hybridization assay conditions as an indication of the presence of *Ureaplasma urealyticum* biotype 1 or *Ureaplasma urealyticum* biotype 2.

79. The method of claim 78, wherein said target nucleic acid sequence is either SEQ ID NO: 126 or SEQ ID NO: 136.

80. The method of claim 78, wherein said target nucleic acid sequence is either SEQ ID NO: 127 or SEQ ID NO: 137.

81. A method for specifically detecting the presence of *Ureaplasma urealyticum* biotype 1 or *Ureaplasma urealyticum* biotype 2 comprising the steps of:

a) contacting a sample with a hybridization assay probe able to hybridize under stringent hybridization assay conditions with either *Ureaplasma urealyticum* biotype 1 or *Ureaplasma urealyticum* biotype 2 nucleic acid to form a detectable probe:target hybrid, wherein said hybridization assay probe does not hybridize to nucleic acid from both *Ureaplasma urealyticum* biotype 1 and *Ureaplasma urealyticum* biotype 2 under said stringent hybridization assay conditions to form said detectable probe:non-target hybrid, said hybridization assay probe

comprising a detection nucleotide base sequence selected from the group consisting of:

SEQ ID NO: 121: CAACACCGAC TCGTTCGAGC,

SEQ ID NO: 122: CAACACCGAC CCATTCGG,

SEQ ID NO: 126: CAACACCGAC UCGUUCGAGC,

SEQ ID NO: 127: CAACACCGAC CCAUUCGG,

SEQ ID NO: 131: GCTCGAACGA GTCGGTGTTG,

SEQ ID NO: 132: CCGAATGGGT CGGTGTTG,

SEQ ID NO: 136: GCUCGAACGA GUCGGUGUUG, and

SEQ ID NO: 137: CCGAAUGGGU CGGUGUUG;

provided that under said stringent hybridization conditions said probe does not hybridize to nucleic acid from *Mycoplasma genitalium, Mycoplasma hominis* and *Mycoplasma pneumoniae* to form a detectable probe:non-target hybrid; and

b) employing said stringent hybridization assay conditions and detecting the presence of said detectable probe:target hybrid formed under said stringent hybridization assay conditions as an indication of the presence of either *Ureaplasma urealyticum* biotype 1 or *Ureaplasma urealyticum* biotype 2.

82. The method of claim **81**, wherein said hybridization assay probe comprises a detection nucleotide base sequence selected from the group consisting of:

SEQ ID NO: 121: CAACACCGAC TCGTTCGAGC,

SEQ ID NO: 126: CAACACCGAC UCGUUCGAGC,

SEQ ID NO: 131: GCTCGAACGA GTCGGTGTTG, and

SEQ ID NO: 136: GCUCGAACGA GUCGGUGUUG.

83. The method of claim **82**, further comprising the use of a helper probe consisting of a sequence selected from the group consisting of:

SEQ ID NO: 123: CGACATTTAA TGATGATCGT TTACGGTGTG GAC,

SEQ ID NO: 125: CCCAGGCACA TCATTTAATG CGTTAGCTA,

SEQ ID NO: 128: CGACAUUUAA UGAUGAUCGU UUACGGUGUG GAC,

SEQ ID NO: 130: CCCAGGCACA UCAUUUAAUG CGUUAGCUA,

SEQ ID NO: 133: GTCCACACCG TAAACGATCA TCATTAAATG TCG,

SEQ ID NO: 135: TAGCTAACGC ATTAAATGAT GTGCCTGGG,

SEQ ID NO: 138: GUCCACACCG UAAACGAUCA UCAUUAAAUG UCG, and

SEQ ID NO: 140: UAGCUAACGC AUUAAAUGAU GUGCCUGGG.

84. The method of claim **81**, wherein said hybridization assay probe comprises a detection nucleotide base sequence selected from the group consisting of:

SEQ ID NO: 122: CAACACCGAC CCATTCGG,

SEQ ID NO: 127: CAACACCGAC CCAUUCGG,

SEQ ID NO: 132: CCGAATGGGT CGGTGTTG, and

SEQ ID NO: 137: CCGAAUGGGU CGGUGUUG.

85. The method of claim **84**, further comprising the use of a helper probe in said step (a), said helper probe consisting of a sequence selected from the group consisting of:

SEQ ID NO: 124: GCCGACATTT AATGATGATC GTTTACGGTG TGGAC,

SEQ ID NO: 125: CCCAGGCACA TCATTTAATG CGTTAGCTA,

SEQ ID NO: 129: GCCGACAUUU AAUGAUGAUC GUUUACGGUG UGGAC,

SEQ ID NO: 130: CCCAGGCACA UCAUUUAAUG CGUUAGCUA,

SEQ ID NO: 134: GTCCACACCG TAAACGATCA TCATTAAATG TCGGC,

SEQ ID NO: 135: TAGCTAACGC ATTAAATGAT GTGCCTGGG,

SEQ ID NO: 139: GUCCACACCG UAAACGAUCA UCAUUAAAUG UCGGC, and

SEQ ID NO: 140: UAGCUAACGC AUUAAAUGAU GUGCCUGGG.

86. The method of any one of claims **82–85**, wherein said hybridization assay probe consists of one or more reporter groups and said detection nucleotide base sequence.

87. A method for detecting the presence of Ureaplasma in a sample and distinguishing said Ureaplasma from *Mycoplasma genitalium, Mycoplasma pneumoniae,* and *Mycoplasma hominis,* comprising the steps of:

a) providing to said sample a hybridization assay probe comprising a nucleotide base sequence selected from the group consisting of

SEQ ID NO: 14: CGTTCGAGCC GACATTTAAT GATGATCG,

SEQ ID NO: 46: CGUUCGAGCC GACAUUUAAU GAUGAUCG,

SEQ ID NO: 47: CGATCATCAT TAAATGTCGG CTCGAACG, and

SEQ ID NO: 48: CGAUCAUCAU UAAAUGUCGG CUCGAACG; wherein under stringent hybridization assay conditions said hybridization assay probe forms a detectable probe:target hybrid with *Ureaplasma urealyticum* nucleic acid, but not with nucleic acid from *Mycoplasma genitalium, Mycoplasma hominis* and *Mycoplasma pneumoniae;* and a helper probe consisting of a nucleotide base sequence selected from the group consisting of:

SEQ ID NO: 13: TTTACGGTGT GGACTACTAG GGTAT,

SEQ ID NO: 15: GCGTTAGCTA CAACACCGAC T,

SEQ ID NO: 85: UUUACGGUGU GGACUACUAG GGUAU,

SEQ ID NO: 86: ATACCCTAGT AGTCCACACC GTAAA,

SEQ ID NO: 87: AUACCCUAGU AGUCCACACC GUAAA,

SEQ ID NO: 88: GCGUUAGCUA CAACACCGAC U,

SEQ ID NO: 89: AGTCGGTGTT GTAGCTAACG C, and

SEQ ID NO: 90: AGUCGGUGUU GUAGCUAACG C; and

b) employing said stringent hybridization assay conditions and detecting the presence of said detectable probe:target hybrid formed under stringent hybridization assay conditions as an indication that Ureaplasma may be present in said sample.

88. The method of claim **87**, wherein said hybridization assay probe consists of one or more reporter groups and a nucleotide base sequence selected from the group consisting of SEQ ID NO: 14, SEQ ID NO: 46, SEQ ID NO: 47, and SEQ ID NO: 48.

89. A method for detecting the presence of Ureaplasma in a sample and distinguishing said Ureaplasma from *Mycoplasma genitalium, Mycoplasma pneumoniae,* and *Mycoplasma hominis* comprising the steps of:

a) providing to said sample a hybridization assay probe comprising a nucleotide base sequence selected from the group consisting of

SEQ ID NO: 17: GCGTCGCAAT AGATGTCAAA CCTAG,

SEQ ID NO: 49: GCGUCGCAAU AGAUGUCAAA CCUAG,

SEQ ID NO: 50: CTAGGTTTGA CATCTATTGC GACGC, and

SEQ ID NO: 51: CUAGGUUUGA CAUCUAUUGC GACGC; wherein under stringent hybridization assay conditions said hybridization assay probe forms a detectable probe:target hybrid with *Ureaplasma urealyticum* nucleic acid, but not with nucleic acid from *Mycoplasma genitalium, Mycoplasma hominis* and *Mycoplasma pneumoniae;* and

a helper probe consisting of a nucleotide base sequence selected from the group consisting of:

SEQ ID NO: 16: GTAAGGTTCT ACGTGTATTG TCAAATTAAG CAACATGCTC CACCAC,

SEQ ID NO: 18: CGACAACCAT GCACCACCTG TCATATTGTT AACCTCAAC,

SEQ ID NO: 91: GUAAGGUUCU ACGUGUAUUG UCAAAUUAAG CAACAUGCUC CACCAC,

SEQ ID NO: 92: GTGGTGGAGC ATGTTGCTTA ATTTGACAAT ACACGTAGAA CCTTAC,

SEQ ID NO: 93: GUGGUGGAGC AUGUUGCUUA AUUUGACAAU ACACGUAGAA CCUUAC,

SEQ ID NO: 94: CGACAACCAU GCACCACCUG UCAUAUUGUU AACCUCAAC,

SEQ ID NO: 95: GTTGAGGTTA ACAATATGAC AGGTGGTGCA TGGTTGTCG, and

SEQ ID NO: 96: GUUGAGGUUA ACAAUAUGAC AGGUGGUGCA UGGUUGUCG; and

b) employing said stringent hybridization assay conditions and detecting the presence of said detectable probe:target hybrid formed under stringent hybridization assay conditions as an indication that Ureaplasma may be present in said sample.

90. The method of claim **89**, wherein said hybridization assay probe consists of one or more reporter groups and a nucleotide base sequence selected from the group consisting of SEQ ID NO: 17, SEQ ID NO: 49, SEQ ID NO: 50, and SEQ ID NO: 51.

91. A hybridization assay probe 10 to 50 nucleotides in length comprising an oligonucleotide sufficiently complementary to a *Ureaplasma urealyticum* target nucleic acid sequence to form a detectable probe:target hybrid with said *Ureaplasma urealyticum* target nucleic acid sequence under stringent hybridization assay conditions, wherein said *Ureaplasma urealyticum* target nucleic acid sequence is selected from the group consisting of:

SEQ ID NO: 31: ACCUCUCAGU ACAGCUACGC G,

SEQ ID NO: 33: CGCGUAGCUG UACUGAGAGG U,

SEQ ID NO: 37: CGUUAAGCAU CUAGAUUUAA UACCAAACUU ACAAACCCG,

SEQ ID NO: 39: CGGGUUUGUA AGUUUGGUAU UAAAUCUAGA UGCUUAACG,

SEQ ID NO: 40: CCUACUACAC UCUAGGUUUA CAGUUUUUGA UACAGCUAGA,

SEQ ID NO: 42: UCUAGCUGUA UCAAAAACUG UAAACCUAGA GUGUAGUAGG,

SEQ ID NO: 43: GUCAGUGAUA GUCCAAGUUG GC,

SEQ ID NO: 45: GCCAACUUUG ACUAUCACUG AC,

SEQ ID NO: 55: GCUAUUUUCG GCUCUAGAGU GCUUUGACUUC UGUGUUCGGG AUG,

SEQ ID NO: 57: CAUCCCGAAC ACAGAAGUCA AGCACUCUAG AGCCGAAAAU AGC,

SEQ ID NO: 58: CGGCUCUAGA GUGCUUGACU UCUGUGUUCG,

SEQ ID NO: 60: CGAACACAGA AGUCAAGCAC UCUAGAGCCG,

SEQ ID NO: 61: CAGUAAUCUA AUUCUCAUUA GACUGAGUUU CCUCAUUUCG,

SEQ ID NO: 63: CGAAUGAGGA AACUCAGUCU AAUGAGAAUU AGAUTUACUG,

SEQ ID NO: 109: GGAUGGGAAC AGGUAUUUCC ACUCUGAUAU GAUCAC, and

SEQ ID NO 111: GUGAUCAUAU CAGAGUGGAA AUACCUGUCC CCAUCC;

wherein under said stringent hybridization assay conditions said hybridization assay probe does not form a detectable probe:non-target hybrid with nucleic acid from *Mycoplasma hominis.*

92. The hybridization assay probe of claim **91**, wherein said hybridization assay probe also does not form said detectable probe:non-target hybrid with nucleic acid from *Mycoplasma genitalium* and *Mycoplasma pneumoniae.*

93. The hybridization assay probe of claim **91**, wherein said hybridization assay probe also does not form said detectable probe:non target hybrid with nucleic acid from *Mycoplasma orale, Mycoplasma fermentans, Mycoplasma capricolum, Mycoplasma lipophilum,* and *Mycoplasma salivarium.*

94. The hybridization assay probe of claim **91**, wherein said target *Ureaplasma urealyticum* nucleic acid sequence is selected from the group consisting of SEQ ID NO: 31 and SEQ ID NO: 33.

95. The hybridization assay probe of claim **91**, wherein said target Ureaplasma urealyticum nucleic acid sequence is selected from the group consisting of SEQ ID NO: 37 and SEQ ID NO: 39.

96. The hybridization assay probe of claim **91**, wherein said target *Ureaplasma urealyticum* nucleic acid sequence is selected from the group consisting of SEQ ID NO: 40 and SEQ ID NO: 42.

97. The hybridization assay probe of claim **91**, wherein said target *Ureaplasma urealyticum* nucleic acid sequence is selected from the group consisting of SEQ ID NO: 43 and SEQ ID NO: 45.

98. The hybridization assay probe of claim **91**, wherein said target *Ureaplasma urealyticum* nucleic acid sequence is selected from the group consisting of SEQ ID NO: 55 and SEQ ID NO: 57.

99. The hybridization assay probe of claim **91**, wherein said target *Ureaplasma urealyticum* nucleic acid sequence is selected from the group consisting of SEQ ID NO: 58 and SEQ ID NO: 60.

100. The hybridization assay probe of claim **91**, wherein said target *Ureaplasma urealyticum* nucleic acid sequence is selected from the group consisting of SEQ ID NO: 61 and SEQ ID NO: 63.

101. The hybridization assay probe of claim **91**, wherein said target *Ureaplasma urealyticum* nucleic acid sequence is selected from the group consisting of SEQ ID NO: 109 and SEQ ID NO: 111.

102. A probe mix comprising:

a) a hybridization assay probe for detecting Ureaplasma under stringent hybridization assay conditions which is 10 to 50 nucleotides in length and comprises a nucleotide base sequence selected from the group consisting of

SEQ ID NO: 2: ACCTCTCAGT ACAGCTACGC G,

SEQ ID NO: 8: CGTTAAGCAT CTAGATTTAA TACCAAACTT ACAAACCCG,

SEQ ID NO: 9: CCTACTACAC TCTAGGTTTA CAGTTTTTGA TACAGCTAGA,

SEQ ID NO: 11: GTCAGTGATA GTCCAAGTTG GC,

SEQ ID NO: 20: CGATTTTGCA GCAGTTTGTA TTAGCCATTG,

SEQ ID NO: 22: GCTATTTTCG GCTCTAGAGT GCTTGACTTC TGTGTTCGGG ATG,

SEQ ID NO: 23: CGGCTCTAGA GTGCTTGACT TCTGTGTTCG,

SEQ ID NO: 26: GGATGGGAAC AGGTATTTCC ACTCTGATAT GATCAC,

SEQ ID NO: 29: CAGTAATCTA ATTCTCATTA GACTGAGTTT CCTCATTCG,

SEQ ID NO: 31: ACCUCUCAGU ACAGCUACGC G,

SEQ ID NO: 32: CGCGTAGCTG TACTGAGAGG T,

SEQ ID NO: 33: CGCGUAGCUG UACUGAGAGG U,

SEQ ID NO: 37: CGUUAAGCAU CUAGAUUUAA UACCAAACUU ACAAACCCG,

SEQ ID NO: 38: CGGGTTTGTA AGTTTGGTAT TAAATCTAGA TGCTTAACG,

SEQ ID NO: 39: CGGGUUUGUA AGUUUGGUAU UAAAUCUAGA UGCUUAACG,

SEQ ID NO: 40: CCUACUACAC UCUAGGUUUA CAGUUUUUGA UACAGCUAGA,

SEQ ID NO: 41: TCTAGCTGTA TCAAAAACTG TAAACCTAGA GTGTAGTAGG,

SEQ ID NO: 42: UCUAGCUGUA UCAAAAACUG UAAACCUAGA GUGUAGUAGG,

SEQ ID NO: 43: GUCAGUGAUA GUCCAAGUUG GC,

SEQ ID NO: 44: GCCAACTTGG ACTATCACTG AC,

SEQ ID NO: 45: GCCAACUUUGG ACUAUCACUG AC,

SEQ ID NO: 52: CGAUUUUGCA GCAGUUUGUA UUAGCCAUUG,

SEQ ID NO: 53: CAATGGCTAA TACAAACTGC TGCAAAATCG,

SEQ ID NO: 54: CAAUGGCUAA UACAAACUGC UGCAAAAUCG,

SEQ ID NO: 55: GCUAUUUUCG GCUCUAGAGU GCUUGACUUC UGUGUUUCGGG AUG,

SEQ ID NO: 56: CATCCCGAAC ACAGAAGTCA AGCACTCTAG AGCCGAAAAT AGC,

SEQ ID NO: 57: CAUCCCGAAC ACAGAAGUCA AGCACUCUAG AGCCGAAAAU AGC,

SEQ ID NO: 58: CGGCUCUAGA GUGCUUGACU UCUGUGUUCG,

SEQ ID NO: 59: CGAACACAGA AGTCAAGCAC TCTAGAGCCG,

SEQ ID NO: 60: CGAACACAGA AGUCAAGCAC UCUAGAGCCG,

SEQ ID NO: 61: CAGUAAUCUA AUUCUCAUUA GACUGAGUUU CCUCAUUUCG,

SEQ ID NO; 62: CGAATGAGGA AACTCAGTCT AATGAGAATT AGATTACTG,

SEQ ID NO: 63: CGAAUGAGGA AACUCAGUCU AAUGAGAAUU AGAUUACUG,

SEQ ID NO: 109: GGAUUGGGAAC AGGUAUUUCC ACUCUGAUAU GAUCAC,

SEQ ID NO: 110: GTGATCATAT CAGAGTGGAA ATACCTGTTC CCATCC, and

SEQ ID NO: 111: GUGAUCAUAU CAGAGUGGAA AUACCUGUUC CCAUCC;

wherein under stringent hybridization assay conditions said hybridization assay probe forms a detectable probe:target hybrid with *Ureaplasma urealyticum* nucleic acid, but does not form a detectable probe:non-target hybrid with nucleic acid from *Mycoplasma genitalium, Mycoplasma hominis* and *Mycoplasma pneumoniae* under said stringent hybridization assay conditions; and

b) a helper probe.

103. The probe mix of claim **102**, wherein said hybridization assay probe comprises a nucleotide base sequence selected from the group consisting of SEQ ID NO: 22, SEQ ID NO: 55, SEQ ID NO: 56, and SEQ ID NO: 57, and said helper probe comprises a nucleotide base sequence selected from the group consisting of:

SEQ ID NO: 24: GGAACAGGTA TTTCCACTCT GATATGATCA CTAC,

SEQ ID NO: 25: GCGTAGCGAT GACCTATTTT ACTTGC,

SEQ ID NO: 103: GGAACAGGUA UUUCCACUCU GAUAUGAUCA CUAC,

SEQ ID NO: 104: GTAGTGATCA TATCAGAGTG GAAATACCTG TTCC,

SEQ ID NO: 105: GUAGUGAUCA UAUCAGAGUG GAAAUACCUG UUCC,

SEQ ID NO: 106: GCGUAGCGAU GACCUAUUUU ACUUGC,

SEQ ID NO: 107: GCAAGTAAAA TAGGTCATCG CTACGC, and

SEQ ID NO: 108: GCAAGUAAAA UAGGUCAUCG CUACGC.

104. The probe mix of claim **103**, wherein said probe mix is selected from the group consisting of:

(a) a probe mix comprising:

a hybridization assay probe consisting of one or more reporter groups and the nucleotide base sequence of either SEQ ID NO: 22 or SEQ ID NO: 55;

a first helper probe consisting of the nucleotide base sequence of either SEQ ID NO: 24 or SEQ ID NO: 103; and

a second helper probe consisting of the nucleotide base sequence of either SEQ ID NO: 25 or SEQ ID NO: 106; and

(b) a probe mix comprising:

a hybridization assay probe consisting of one or more reporter groups and the nucleotide base sequence of either SEQ ID NO: 56 or SEQ ID NO: 57;

a first helper probe consisting of the nucleotide base sequence of either SEQ ID NO: 104 or SEQ ID NO. 105; and

a second helper probe consisting of the nucleotide base sequence of either SEQ ID NO: 107 or SEQ ID NO: 108.

105. The probe mix of claim **102**, wherein said hybridization assay probe comprises a nucleotide base sequence selected from the group consisting of SEQ ID NO: 23, SEQ ID NO: 58, SEQ ID NO: 59, and SEQ ID NO: 60, and said helper probe comprises a nucleotide base sequence selected from the group consisting of

SEQ ID NO: 26: GGATGGGAAC AGGTATTTCC ACTCTGATAT GATCAC,

SEQ ID NO: 27: GCGTAGCGAT GACCTATTTT ACTTGCGCTA TTTT,

SEQ ID NO: 109: GGAUGGGAAC AGGUAUUUCC ACUCUGAUAU GAUCAC,

SEQ ID NO: 110: GTGATCATAT CAGAGTGGAA ATACCTGTTC CCATCC,

SEQ ID NO: 111: GUGAUCAUAU CAGAGUGGAA AUACCUGUUC CCAUCC,

SEQ ID NO: 112: GCGUAGCGAU GACCUAULUU ACUUGCGCUA UUU,

SEQ ID NO: 113: AAAATAGCGC AAGTAAAATA GGTCATCGCT ACGC, and

SEQ ID NO: 114: AAAAUAGCGC AAGUAAAAUA, GGUCAUCGCU ACGC.

106. The probe mix of claim **105**, wherein said probe mix is selected from the group consisting of:

(a) a probe mix comprising:

a hybridization assay probe consisting of one or more reporter groups and the nucleotide base sequence of either SEQ ID NO: 23 or SEQ ID NO: 58;

a first helper probe consisting of the nucleotide base sequence of either SEQ ID NO: 26 or SEQ ID NO: 109; and

a second helper probe consisting of the nucleotide base sequence of either SEQ ID NO: 27 or SEQ ID NO: 112; and

(a) a probe mix comprising:

a hybridization assay probe consisting of one or more reporter groups and the nucleotide base sequence of either SEQ ID NO: 59 or SEQ ID NO: 60;

a first helper probe consisting of the nucleotide base sequence of either SEQ ID NO: 110 or SEQ IDNO: 111; and

a second helper probe consisting of the nucleotide base sequence of either SEQ ID NO: 113 or SEQ ID NO: 114.

107. A hybridization assay probe 10 to 100 nucleotides in length comprising an oligonucleotide sufficiently complementary to a *Ureaplasma urealyticum* target nucleic acid sequence to form a detectable probe:target hybrid with said *Ureaplasma urealyticum* target nucleic acid sequence under stringent hybridization assay conditions, wherein said *Ureaplasma urealyticum* target nucleic acid sequence is SEQ ID NO: 54: CAAUGGCUAA UACAAACUGC UGCAAAAUCG, and said hybridization assay probe targets at least one nucleotide 5' to "A" at nucleotide position 11 in SEQ ID NO: 54, wherein under said stringent hybridization assay conditions said hybridization assay probe does not form a detectable probe:non-target hybrid with nucleic acid from *Mycoplasma hominis*.

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